

| L Number | Hits | Search Text | DB | Time stamp |
|----------|------|---|---|------------------|
| 1 | 6 | cory NEAR suzanne | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:36 |
| 2 | 107 | bcl NEAR w | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:34 |
| 3 | 4 | "5789201" | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:34 |
| 4 | 2 | "5883229" | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:34 |
| 11 | 6 | Guastella NEAR John | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:35 |
| 12 | 2 | Holmgreen NEAR Shaun | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:37 |
| 15 | 97 | (bcl NEAR w) and apoptosis | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:38 |
| 16 | 28 | ((bcl NEAR w) and apoptosis) and bcl\$3.clm. | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:39 |
| 17 | 8 | bcl-w.clm. | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2004/03/29 14:40 |
| 18 | 10 | (US-5883229-\$ or US-5789201-\$).did. or (US-20020119943-\$ or US-20040014218-\$).did. or (WO-9735971-\$ or WO-9914321-\$ or WO-9913710-\$ or WO-9115116-\$).did. or (WO-9913710-\$ or US-20020119943-\$).did. | USPAT; US-PGPUB; EPO; DERWENT | 2004/03/29 14:40 |

=> d his

(FILE 'HOME' ENTERED AT 14:41:41 ON 29 MAR 2004)

FILE 'MEDLINE, CANCERLIT, SCISEARCH, CAPLUS' ENTERED AT 14:42:01 ON 29 MAR 2004

E CORY S?/AU
L1 124 S E11
L2 416 S E1
L3 540 S L1 OR L2
L4 186 S L3 AND BCL?
L5 29 S L4 AND BCL-W
L6 10 DUP REM L5 (19 DUPLICATES REMOVED)
L7 10 SORT L6 PY
L8 79913 S BCL?
L9 318 S L8 AND BCL-W
L10 16 S L9 AND PY<=1997
L11 6 DUP REM L10 (10 DUPLICATES REMOVED)
L12 6 SORT L11 PY

=> d an ti so au ab pi 17 3 8 1 4 7 9

L7 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:650444 CAPLUS
DN 127:327462
TI A novel mammalian gene, **bcl-w**, belongs to the
bcl-2 family of apoptosis-controlling genes
SO PCT Int. Appl., 85 pp.
CODEN: PIXXD2
IN **Cory, Suzanne**; Adams, Jerry McKee; Gibson, Leonie M.; Holmgreen,
Shaun P.
AB Human and mouse cDNAs for **bcl-2**-related gene **bcl-w** and the corresponding proteins are disclosed. The present invention is broadly directed to therapeutic mols. capable of inter alia modulating apoptosis in mammalian cells. The therapeutic mols. of the present invention encompass genetic sequences and chemical entities capable of regulating expression of **bcl-w** family and which promotes cell survival. The therapeutic mols. of the present invention may have further utility in delaying cell cycle entry. In addition, the present invention extends to chemical entities capable of modulating activity and function of the translation product of the **bcl-w** gene. The present invention also extends to the translation product of the **bcl-w** gene and its use in, for example, therapy, diagnosis, antibody generation and, as a screening tool for therapeutic mols. capable of modulating physiol. cell death or survival and/or modulating cell cycle entry. The **bcl-w** gene was mapped to human chromosome 14q11.2. Alternative splicing of the **bcl-w** gene transcript produced an mRNA for a **bcl-w-rox** chimera. The **bcl-w** gene was expressed in many cell types. Amongst the tissues surveyed, the level was highest in brain, colon and salivary gland. A survey of 50 mouse hemopoietic cell lines revealed that **bcl-w** expression was common in cells of several myeloid lineages, including macrophage, megakaryocyte, erythroid and mast cell lines, but rare in either B or T lymphoid lines.

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|--|----------|-----------------|----------|
| ----- | --- | ----- | ----- | ----- |
| PI WO 9735971 | A1 | 19971002 | WO 1997-AU199 | 19970327 |
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| CA 2250207 | AA | 19971002 | CA 1997-2250207 | 19970327 |
| AU 9721439 | A1 | 19971017 | AU 1997-21439 | 19970327 |
| AU 728863 | B2 | 20010118 | | |

STN: SEARCH HISTORY

EP 932674 A1 19990804 EP 1997-913986 19970327
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO
 JP 2000513566 T2 20001017 JP 1997-533874 19970327
 US 2002119943 A1 20020829 US 2001-925674 20010809

L7 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:215553 CAPLUS

DN 130:235990

TI Animals carrying **bcl-w** mutations and their use in the study of male infertility

SO PCT Int. Appl., 52 pp.

CODEN: PIXXD2

IN **Cory, Suzanne**; Adams, Jerry; Print, Cris; Gibson, Leonie; Koentgen, Frank

AB Transgenic mice carrying a disruption of the **bcl-w** gene or of genes interacting with it and that fail to undergo productive spermatogenesis and are male infertile are described for use in studies of male fertility and of the biol. role of **bcl-w**. Such animals can be used to screen for therapeutic mols. including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in said animals as well as a model for mols. and genetic sequences which can induce infertility. The **bcl-w** gene was disrupted by insertional inactivation. Inactivation of **bcl-w** did not affect survival of fetal and neonatal mice and the mutation showed a near-normal Mendelian segregation. Hematopoiesis was unaffected by the mutation but the testes showed heterogeneous pathol. changes in the seminiferous tubules. Sertoli cells remained normal although low in number and Leydig cell were increased by 50%. Germ cell nos. declined steadily with as the stage of development advanced. The mutation did not affect androgen levels or androgen responses in other organs.

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|------------|---|--|-----------------|----------|
| PI | WO 9913710 | A1 | 19990325 | WO 1998-AU764 | 19980916 |
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| | AU 9890557 | A1 | 19990405 | AU 1998-90557 | 19980916 |
| | AU 757728 | B2 | 20030306 | | |
| | EP 1011319 | A1 | 20000628 | EP 1998-942391 | 19980916 |
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L7 ANSWER 1 OF 10 MEDLINE on STN

AN 96358615 MEDLINE

TI **bcl-w**, a novel member of the **bcl-2** family, promotes cell survival.

SO Oncogene, (1996 Aug 15) 13 (4) 665-75.

Journal code: 8711562. ISSN: 0950-9232.

AU Gibson L; Holmgreen S P; Huang D C; Bernard O; Copeland N G; Jenkins N A; Sutherland G R; Baker E; Adams J M; **Cory S**

AB The prototypic mammalian regulator of cell death is **bcl-2**, the oncogene implicated in the development of human follicular lymphoma. Several homologues of **bcl-2** are now known. Using a PCR-based strategy we cloned a novel member of this gene family, denoted **bcl-w**. The gene, which is highly conserved between mouse and human, resides near the T-cell antigen receptor alpha gene within the central portion of mouse chromosome 14 and on human chromosome 14 at band q11. Enforced expression of **bcl-w** rendered lymphoid and myeloid cells refractory to several (but not all) cytotoxic conditions. Thus, like **Bcl-2** and **Bcl-x**, the **Bcl-w** protein promotes cell survival, in contrast to

other close homologues, Bax and Bak, which facilitate cell death. Comparison of the expected amino acid sequence of **Bcl-w** with that of these relatives helps to delineate residues likely to convey survival or anti-survival function. While expression of **bcl-w** was uncommon in B or T lymphoid cell lines, the mRNA was observed in almost all murine myeloid cell lines analysed and in a wide range of tissues. These findings suggest that **bcl-w** participates in the control of apoptosis in multiple cell types. Its functional similarity to **bcl-2** also makes it an attractive candidate proto-oncogene.

L7 ANSWER 4 OF 10 MEDLINE on STN
 AN 1998445387 MEDLINE
 TI Apoptosis regulator **bcl-w** is essential for spermatogenesis but appears otherwise redundant.
 SO Proceedings of the National Academy of Sciences of the United States of America, (1998 Oct 13) 95 (21) 12424-31.
 Journal code: 7505876. ISSN: 0027-8424.
 AU Print C G; Loveland K L; Gibson L; Meehan T; Stylianou A; Wreford N; de Kretser D; Metcalf D; Kontgen F; Adams J M; **Cory S**
 AB Proteins of the **Bcl-2** family are important regulators of apoptosis in many tissues of the embryo and adult. The recently isolated **bcl-w** gene encodes a pro-survival member of the **Bcl-2** family, which is widely expressed. To explore its physiological role, we have inactivated the **bcl-w** gene in the mouse by homologous recombination. Mice that lack **Bcl-w** were viable, healthy, and normal in appearance. Most tissues exhibited typical histology, and hematopoiesis was unaffected, presumably due to redundant function with other pro-survival family members. Although female reproductive function was normal, the males were infertile. The testes developed normally, and the initial, prepubertal wave of spermatogenesis was largely unaffected. The seminiferous tubules of adult males, however, were disorganized, contained numerous apoptotic cells, and produced no mature sperm. Both Sertoli cells and germ cells of all types were reduced in number, the most mature germ cells being the most severely depleted. The **bcl-w**^{-/-} mouse provides a unique model of failed spermatogenesis in the adult that may be relevant to some cases of human male sterility.

L7 ANSWER 7 OF 10 MEDLINE on STN
 AN 1999310955 MEDLINE
 TI Survival activity of **Bcl-2** homologs **Bcl-w** and **A1** only partially correlates with their ability to bind pro-apoptotic family members.
 SO Cell death and differentiation, (1999 Jun) 6 (6) 525-32.
 Journal code: 9437445. ISSN: 1350-9047.
 AU Holmgren S P; Huang D C; Adams J M; **Cory S**
 AB Certain **Bcl-2** family members promote cell survival, whereas others promote apoptosis. To explore further how heterodimerization of opposing members affects survival activity, we have compared the abilities of the anti-apoptotic **Bcl-w** and **A1** to bind to the pro-apoptotic Bax, Bak, Bad and Bik and to protect cells from their cytotoxic action. **Bcl-w** co-immunoprecipitated from cell lysates with Bax, Bak, Bad and Bik, but **A1** bound only Bak and Bik. Mutation of **A1** at a highly conserved glycine within the BH1 domain prevented binding, but the comparable **Bcl-w** mutant still bound Bak, Bad and Bik, indicating that the glycine is not essential for all heterodimerization. **Bcl-w** and **A1** protected against apoptosis induced by over-expression of Bax or Bad but not that induced by Bak or Bik. With several gene pairs, binding and protection were discordant. The results may reflect critical threshold affinities but also suggest that certain pro-apoptotic proteins may also contribute to apoptosis by a mechanism independent of binding pro-survival proteins.

L7 ANSWER 9 OF 10 MEDLINE on STN
 AN 2001360165 MEDLINE
 TI Tissue expression and subcellular localization of the pro-survival molecule **Bcl-w**.
 SO Cell death and differentiation, (2001 May) 8 (5) 486-94.

Journal code: 9437445. ISSN: 1350-9047.

AU O'Reilly L A; Print C; Hausmann G; Moriishi K; Cory S; Huang D
C; Strasser A

AB Anti-apoptotic members of the Bcl-2 family, such as Bcl-w, maintain cell viability by preventing the activation of the cell death effectors, the caspases. Gene targeting experiments in mice have demonstrated that Bcl-w is required for spermatogenesis and for survival of damaged epithelial cells in the gut. Bcl-w is, however, dispensable for physiological cell death in other tissues. Here we report on the analysis of Bcl-w protein expression using a panel of novel monoclonal antibodies. Bcl-w is found in a diverse range of tissues including colon, brain and testes. A survey of transformed cell lines and purified hematopoietic cells demonstrated that Bcl-w is expressed in cells of myeloid, lymphoid and epithelial origin. Subcellular fractionation and confocal laser scanning microscopy demonstrated that Bcl-w protein is associated with intracellular membranes. The implications of these results are discussed in the context of the phenotype of Bcl-w-null mice and recent data that suggest that Bcl-w may play a role in colon carcinogenesis.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:01:08 ; Search time 2762.74 seconds

(without alignments)
9146.355 Million cell updates/sec

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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DEFINITION Sequence 6 from Patent EP0932674.

ACCESSION AX022529

VERSION AX022529.1 GI:10046125

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.

A novel mammalian gene, bcl-2, belongs to the bcl-2 family of

apoptosis-controlling genes

Patent: EP 0932674-A 6 04-AUG-1999;

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ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL

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Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAWN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
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ORIGIN

Query Match 100.0%; Score 583; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.4e-121; Mismatches 0; Indels 0; Gaps 0;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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541 GGGGCGCTGTGTAAGTGAAGGGGCTTTTGTCTAGCAAGTGA 583

RESULT 3
AX481423 582 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 37 from Patent WO02055693.
DEFINITION AX481423

ACCESSION AX481423
VERSION AX481423.1 GI:22316337
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kreutzer, R., Jilmer, S., Post, S. and Hadwiger, P.
METHOD for inhibiting the expression of a target gene
Parent: WO 02055693-A 37 18-UTR-2002;
JOURNAL
Ridopharma AG (DE)
FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 4.8e-120;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCGACCCCGAGCTCGGCCCAAGACACAGGAGCTCTGTGCGAGACTTTGTAGATTAT 60
DB 1 ATGGCGACCCCGAGCTCGGCCCAAGACACAGGAGCTCTGTGCGAGACTTTGTAGATTAT 60
QY 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGAGCTGCCCCGGGAGAGGCCCAAGAGCTGAC 120
DB 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGAGCTGCCCCGGGAGAGGCCCAAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCGATCGGGGAGCTGAGAGATGATTCAGACCGGCTTCCGGCGAC 180
DB 121 CCGCTGACACCAAGCGATCGGGGAGCTGAGAGATGATTCAGACCGGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCCAAGCTCAGCCCAAGAGCTTACC 240
DB 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCCAAGCTCAGCCCAAGAGCTTACC 240
QY 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGCTTGTAGCTTTT 300
DB 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGCTTGTAGCTTTT 300
QY 301 CTCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGGGA 360
DB 301 GTCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGGGA 360
QY 361 CAAAGTGCAGAGTGAATGATGAGCTTACCTGAGACGCGGCTGCTGATTCAGAGC 420
DB 361 CAAAGTGCAGAGTGAATGATGAGCTTACCTGAGACGCGGCTGCTGATTCAGAGC 420
QY 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATACGGGAGCGGGGCGCTTGGAGAGCGCG 480
DB 421 AGTGGGGGCTGGGCGAGTTCAAGCTCTATACGGGAGCGGGGCGCTTGGAGAGCGCG 480
QY 481 CGTCTGCGGAGGAGGAACTGGGCAATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTG 540
DB 481 CGTCTGCGGAGGAGGAACTGGGCAATCAGTGAAGACAGTGTGACGGGGCGCTGGCACTG 540
QY 541 GGGGGCCCTGTAATCTTAAGGGGCTTTTGTCTAGCAAGTGA 582
DB 541 GGGGGCCCTGTAATCTTAAGGGGCTTTTGTCTAGCAAGTGA 582
RESULT 4
LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59747
VERSION U59747.1 GI:1572492
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
JOURNAL
MEDLINE
PUBMED
8761287
REFERENCE
2 (bases 1 to 582)
Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
Cory, S.
Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q11"
1..582
/gene="bcl-w"
/note="Promotes cell survival"
/codon_start=1
/product="Bcl-w"
/protein_id="AAB09055.1"
/db_xref="GI:1572492"
/translation="MAYTASAPDTRALVADTVGYKLRKGYVCGAGPBPAAPIHQ
AMRAAGDEFETFRFTSDLAQLHVTGSAQDRFTQVDFQGGPWWVAFV
GAALCAESVNMKEPVLGVQVEMVAVLETRLDWIHSSGMAEFTALYGDALBEAR
RLREGNMVASVRLTGAVALGALTVGAFPAK"
ORIGIN
Query Match 99.0%; Score 577.2; DB 9; Length 582;
Best Local Similarity 99.5%; Pred. No. 4.8e-120;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCGACCCCGAGCTCGGCCCAAGACACAGGAGCTCTGTGCGAGACTTTGTAGATTAT 60
DB 1 ATGGCGACCCCGAGCTCGGCCCAAGACACAGGAGCTCTGTGCGAGACTTTGTAGATTAT 60
QY 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGAGCTGCCCCGGGAGAGGCCCAAGAGCTGAC 120
DB 61 AAGCTGAGGCGAAGAGGTTATCTGTGAGAGCTGCCCCGGGAGAGGCCCAAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCGATCGGGGAGCTGAGAGATGATTCAGACCGGCTTCCGGCGAC 180
DB 121 CCGCTGACACCAAGCGATCGGGGAGCTGAGAGATGATTCAGACCGGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCCAAGCTCAGCCCAAGAGCTTACC 240
DB 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCCAAGCTCAGCCCAAGAGCTTACC 240
QY 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGCTTGTAGCTTTT 300
DB 241 CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCCAAGCTGGGGCGCTTGTAGCTTTT 300
QY 301 CTCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGGGA 360
DB 301 GTCTTTGGGGCTGACATGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGGGA 360
QY 361 CAAAGTGCAGAGTGAATGATGAGCTTACCTGAGACGCGGCTGCTGATTCAGAGC 420
DB 361 CAAAGTGCAGAGTGAATGATGAGCTTACCTGAGACGCGGCTGCTGATTCAGAGC 420
QY 421 AGTGGGGGCTGGGCGAGTTCAGCTCTATACGGGAGCGGGGCGCTTGGAGAGCGCG 480
DB 421 AGTGGGGGCTGGGCGAGTTCAGCTCTATACGGGAGCGGGGCGCTTGGAGAGCGCG 480

QY 481 CGTCTGCGGAGGAGGAACTGAGCATCACTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
DB 481 CCGTCTGCGGAGGAGGAACTGAGCATCACTGAGGACAGTGTGACGGGGCCGTGGCACTG 540
QY 541 GGGGCGCCCTGTACTGTGTAGGGGCTTTTGTGTAGCACTGA 582
DB 541 GGGGCGCCCTGTACTGTGTAGGGGCTTTTGTGTAGCACTGA 582

RESULT 5
DB7461 3542 bp mRNA linear PRI 06-OCT-2001
LOCUS DB7461 Human mRNA for KIAA0271 gene, complete cds.
DEFINITION DB7461
ACCESSION DB7461.1 GI:1944417
VERSION DB7461.1
KEYWORDS KIAA0271.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,
AUTHORS Ohara,O., Tanaka,A., Kofani,H., Miyajima,N. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain
JOURNAL DNA Res. 3 (5), 321-329 (1996)
MEDLINE 97191544
PUBMED 9039502
REFERENCE 2 (bases 1 to 3542)
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
TITLE Direct Submission
SUBMITTED (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute,
1532-3, Yana, Atsuzaki, Chiba 292-0812, Japan
JOURNAL (E-mail:cdna@kazusa.or.jp, Tel:+81-438-52-3913)
FEATURES
source Location/Qualifiers
1..3542
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HA6752"
/sex="male"
/cell_line="KG-1"
/cell_type="myoblast"
/tissue_type="brain"
/clone_1b="pSPORT 1"
1..3542
/gene="KIAA0271"
177..759
/gene="KIAA0271"
/note="similar to human transforming protein bcl-2
(A24428)"
/codon_start=1
/protein_id="BAAL9666.1"
/db_xref="GI:1944418"
/translation="MATEPSADPTPALVADYGVYLRKQYVCGAPSPADPLHQ
AMRAGDEFEKFRFRFSDLAQLHVTGPSAQRTQVSDLPQGPWGLVAFVF
GAALCAESVNEKEMPELVGVQVEMVAVYETRLADVIHSSGMAEFTALYGGALEEAR
RLREGNMAVSRIVLTGVALGALVTVGAFFPAK"

ORIGIN
Query Match 98.6%; Score 575; DB 9; Length 3542;
Best Local Similarity 99.1%; Pred. No. 1.2e-119;
Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGACCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 60
DB 177 ATGGCGACCCCGACCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGTTAT 236
QY 61 AAGCTGAGGAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCACAGCACTGAC 120
DB 237 AAGCTGAGGAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCACAGCACTGAC 296

QY 121 CCGCTCCACCAAGCCATGCGGGAGCTGGAGATGATGGAGACCCGCTTCGGGGGAC 180
DB 297 CCGCTCCACCAAGCCATGCGGGAGCTGGAGATGATGGAGACCCGCTTCGGGGGAC 356
QY 181 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 240
DB 357 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 416
QY 241 CAGGTCTCCGACCAACTTTTTCAGGGGGCCCCCACTGGGGCGGCTTTAGCTTTCTT 300
DB 417 CAGGTCTCCGACCAACTTTTTCAGGGGGCCCCCACTGGGGCGGCTTTAGCTTTCTT 476
QY 301 CTCTTTGGGCGTGCACCTGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGG 360
DB 477 GTCTTTGGGCGTGCACCTGTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGGTGG 536
QY 361 CAGTGCAGAGATGATGATGATGCTTACCTGGAGACGCGGCTGTGACTGATCCACAC 420
DB 537 CAGTGCAGAGATGATGATGATGCTTACCTGGAGACGCGGCTGTGACTGATCCACAC 596
QY 421 AGTGGGGGCTGGGCGGAGTTCAAGCTTATACGGGAGACGGGCGCTGGAGAGGCGCG 480
DB 597 AGTGGGGGCTGGGCGGAGTTCAAGCTTATACGGGAGACGGGCGCTGGAGAGGCGCG 656
QY 481 CGTCTGCGGAGGGGAACTGGGATCAGTGAAGACAGTGTGAACGGGGGCGCTGGCACTG 540
DB 657 CGTCTGCGGAGGGGAACTGGGATCAGTGAAGACAGTGTGAACGGGGGCGCTGGCACTG 716
QY 541 GGGGCGCTGTACTGTAGGGGCTTTTGTGTAGCAAGTGA 583
DB 717 GGGGCGCTGTACTGTAGGGGCTTTTGTGTAGCAAGTGA 759

RESULT 6
AR020780 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020780
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Giustella,J.
TITLE Gene coding for bcl-2 homolog
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
FEATURES
source Location/Qualifiers
1..579
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 97.4%; Score 567.8; DB 6; Length 579;
Best Local Similarity 98.8%; Pred. No. 6.4e-118;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 61 AAGTGAAGGAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCACAGAGCTGAC 120
DB 61 AAGTGAAGGAGAAAGGTTATGTCGTGAGCTGGCCCCGGGAGAGGCCACAGAGCTGAC 120
QY 121 CCGGTGACCAAGCAATGCGGGCAGCTGAGATGAGTTGAGAACCGGCTTCGCGCGCAC 180
DB 121 CCGGTGACCAAGCAATGCGGGCAGCTGAGATGAGTTGAGAACCGGCTTCGCGCGCAC 180
QY 181 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 240
DB 181 TTCTGTGATCTGGCGGCTAGCTGATGATGACCCCAAGGCTCAGCCAGCAAGCTTACC 240

QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTTCTT 300
Db 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCCCACTGGGGCCGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTGACTGTGTGCTGAGAGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGACTGTGTGCTGAGAGTCAACAAGGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTCGAGAGTGTGATGTGTGCTTACCTGAGACCGGGCTGTGCTGACTGTGATCCACAGC 420
Db 361 CAAGTCGAGAGTGTGATGTGTGCTTACCTGAGACCGGGCTGTGCTGACTGTGATCCACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGGGCGG 480
Db 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGGGCGG 480
QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCCTGGCACTG 540
Db 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCCTGGCACTG 540
QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 579
Db 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAG 579

RESULT 7
AF096291 582 bp mRNA linear ROD 28-FEB-2000

LOCUS AF096291 Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
DEFINITION AF096291
VERSION AF096291.1 GI:3747129

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 582)
AUTHORS Hammer, S., Skoglova, Y. and Lindholm, D.
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
JOURNAL Neuroscience 91 (2), 673-684 (1999)

REFERENCE 2 (bases 1 to 582)
AUTHORS Hammer, S., Skoglova, Y. and Lindholm, D.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden

FEATURES
source
1..582
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="postnatal"
1..582
/gene="bcl-w"
1..582
/gene="bcl-w"
/note="Bcl-2 family member"
/codon_start=1
/product="Bcl-w"
/protein_id="AA064200.1"
/db_xref="GI:3747130"
/translation="WATPASTPDTALVADFGVYKIRQKGYVCGAGPBGSPADPLHQ
AMRAAGDEFTFRRTFSDLAQLHVTGSAQGRFTQVSEDLFGQGPNNGRVAFVFF
GAALCAESVKNEMEPVGVQVDMVTYLETRLADWTHSSGMAEFALVGDGLEEAR
RLRGNMAVRVLTGAVLALVTVGAFAASK"

ORIGIN
1..1110
/organism="Rattus norvegicus"

Query Match 90.5%; Score 527.6; DB 10; Length 582;
Best Local Similarity 94.2%; Pred. No. 7.7e-109;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGGCAACCCAGCTCGGGCCCAAGACACAGGGGCTGTGTGAGACTTTGATGAT 60
Db 1 ATGGGCAACCCAGCTCGGGCCCAAGACACAGGGGCTGTGTGAGACTTTGATGAT 60
QY 61 AAGCTGAGCAAGAAAGGTTATGTGTGAGACTGTGAGCTGGGGAGGGCCAGAGCTGAC 120
Db 61 AAGCTGAGCAAGAAAGGTTATGTGTGAGACTGTGAGCTGGGGAGGGCCAGAGCTGAC 120
QY 121 CCGCTGACCAAGCCTGCGGCAAGCTGAGATAGTTTCAAGACCCGCTTCCGCGCAC 180
Db 121 CCGCTGACCAAGCCTGCGGCAAGCTGAGATAGTTTCAAGACCCGCTTCCGCGCAC 180
QY 181 TTCTGTATCTGGGGGCTGAGCTGATGTGACCCAGGCTGAGCCAGCAAGCTTGACC 240
Db 181 TTCTGTATCTGGGGGCTGAGCTGATGTGACCCAGGCTGAGCCAGCAAGCTTGACC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTTCTT 300
Db 241 CAGGCTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTTCTT 300
QY 301 CTCTTTGGGGCTGACTGTGTGCTGAGAGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGACTGTGTGCTGAGAGTCAACAAGGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTCGAGAGTGTGATGTGTGCTTACCTGAGACCGGGCTGTGCTGACTGTGATCCACAGC 420
Db 361 CAAGTCGAGAGTGTGATGTGTGCTTACCTGAGACCGGGCTGTGCTGACTGTGATCCACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGGGCGG 480
Db 421 AGTGGGGGCTGGGGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGAGAGAGGGCGG 480
QY 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCCTGGCACTG 540
Db 481 CGTCTGCGGAGAGGGGAACTGGGCATCAGTGAAGACAGTGTGACGGGGCCCTGGCACTG 540
QY 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAGTGA 582
Db 541 GGGGCCCTGGTAACTGTAGGGGCTTTTGTAGGCAAGTGA 582

RESULT 8
AY185100 1110 bp mRNA linear ROD 24-JUN-2003

LOCUS AY185100 Rattus norvegicus BCL-WEL mRNA, complete cds.
DEFINITION AY185100
VERSION AY185100.1 GI:32185284

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh, T., Itoh, A. and Pleasure, D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)

REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh, T., Itoh, A. and Pleasure, D.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Neurology Research. The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA

FEATURES
source
1..1110
/organism="Rattus norvegicus"

RESULT 10
LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5789201.
ACCESSION AR020779
VERSION AR020779.1 GI:3975394
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 579)
AUTHORS Guasteira,J.
TITLE Genes coding for bcl-2 and bcl-2 homologues
JOURNAL Patent: US 5789201-A 1 04-Aug-1998;
FEATURES location/Qualifiers
source 1. 579
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 89.7%; Score 523; DB 6; Length 579;
Best Local Similarity 94.0%; Pred. No. 8.5e-108;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGAGCTCGCCCGACAGACAGCGGCTCTGGTGGCAGACTTTGAGTTAT 60
Db 1 ATGGCGACCCGAGCTCGCCCGACAGACAGCGGCTCTGGTGGCAGACTTTGAGTTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGAGCTGAGCCCGGAGAGGCGCCAGAGCTGAC 120
Db 61 AAGCTGAGAGAGAGGTTATGCTGTGAGAGCTGAGCCCGGAGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGATGATTGAGACCCGCTTCCGCGCAGC 180
Db 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGATGATTGAGACCCGCTTCCGCGCAGC 180
QY 181 TTCTCTATGCTGGGGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAACGCTTCACC 240
Db 181 TTCTCTATGCTGGGGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAACGCTTCACC 240
QY 241 CAGGCTCTCCGACGAATTTTCAAGGGGGCCCACTGAGGGCGCTTGTAGGCTTCTTT 300
Db 241 CAGGCTCTCCGACGAATTTTCAAGGGGGCCCACTGAGGGCGCTTGTAGGCTTCTTT 300
QY 301 CTCTTTGGGGGCTGACATGCTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGCTGGA 360
Db 301 GTCTTTGGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAGATGAAACCACTGCTGGA 360
QY 361 CAAGTGCAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CAAGTGCAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTAATCGGGGAGCGGGGCGCTGGAGGAGGCGCG 480
Db 421 AGTGGGGGCTGGGGGAGTTTCAAGCTCTAATCGGGGAGCGGGGCGCTGGAGGAGGCGCG 480
QY 481 CGTGTGCGGAGGAGGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 CGTGTGCGGAGGAGGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GGGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
Db 541 GGGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579

RESULT 11
LOCUS MMU59746 582 bp mRNA linear ROD 29-SEP-1996
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59746
VERSION U59746.1 GI:1572494
KEYWORDS

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M., and Cory,S.
TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival
JOURNAL Oncogene 13 (4), 665-675 (1996)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
FEATURES location/Qualifiers
source 1. 582
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="14"
/cell_line="Bar3"
/gene="bcl-w"
1. 582
/note="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
/codon_start=1
/product="Bcl-w"
/protein_id="AAB05056.1"
/db_xref="GI:1572494"
/translation="MARPASPTDRLAVDFVGYKLRQGYVCGAPGEGPADPLHQ
AMRAAGDEFERFRFTFSDLAOLHTFPGSQOFTQVSDLPFGSPWGRVLVAFVY
GAALCAESVKNKEPLVGOVDMVAYLETSLADIMHSSGMAEFYALYDGALEEAR
RLRSNMASVATVLTGVALGALVTVGAFPSK"

ORIGIN
Query Match 89.7%; Score 522.8; DB 10; Length 582;
Best Local Similarity 93.6%; Pred. No. 9.4e-108;
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGAGCTCGCCCGACAGACAGCGGCTCTGGTGGCAGACTTTGAGTTAT 60
Db 1 ATGGCGACCCGAGCTCGCCCGACAGACAGCGGCTCTGGTGGCAGACTTTGAGTTAT 60
QY 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGAGCTGAGCCCGGAGAGGCGCCAGAGCTGAC 120
Db 61 AAGCTGAGGAGAGAGGTTATGCTGTGAGAGCTGAGCCCGGAGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGATGATTGAGACCCGCTTCCGCGCAGC 180
Db 121 CCGCTGACACCAAGCCATGCGGCGAGCTGAGAGATGATTGAGACCCGCTTCCGCGCAGC 180
QY 181 TTCTCTGATGCTGGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TTCTCTGATGCTGGGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CAGGCTCTCCGACGAATTTTCAAGGGGGCCCACTGAGGGCGCTTGTAGGCTTCTTT 300
Db 241 CAGGCTCTCCGACGAATTTTCAAGGGGGCCCACTGAGGGCGCTTGTAGGCTTCTTT 300
QY 301 CTCTTTGGGGGCTGACATGCTGTGCTGAGAGTGTCAACAAGAGATGAAACCACTGCTGGA 360
Db 301 GTCTTTGGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAGATGAAACCACTGCTGGA 360
QY 361 CAAGTGCAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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| AUTHORS | | | |
| TITLE | | | |
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| Qy | 241 | CAGGTCCGAGGAACTTTTCAAGGGGGCCCAACTGAGGGCCGCTGTAGCTTCTTT | 300 |
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| Qy | 421 | AGTGGGGGCTGGGGGAGTTCAAGTCTATACGGGGAGCGGGCCCTGAGAGAGCGGG | 480 |
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| TITLE | | | |
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ORIGIN

Query Match 87.5%; Score 510; DB 10; Length 3473;
Best Local Similarity 92.3%; Pred. No. 5.9e-105;
Matches 537; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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RESULT 14
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DEFINITION Sequence 8 from Patent BP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

REFERENCE unclassified.
1 Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
AUTHORS
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL apoptosis-controlling genes
PATENT: EP 0932674-A 8 04-AUG-1999;
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ORIGIN

Query Match 85.9%; Score 501; DB 6; Length 581;
Best Local Similarity 91.4%; Pred. No. 7.9e-103;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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VERSION AX030819.1 GI:10046127
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL

unidentified
unidentified
unclassified.

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Adams, J.M., Holmgren, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKER (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
Location/Qualifiers

FEATURES
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ORIGIN

Query Match 85.9%; Score 501; DB 6; Length 581;
Best Local Similarity 91.4%; Pred. No. 7.9e-103;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGCGACCCCAAGCTCGGCCCCAGACACACGCGCTCTGTGCGACACTTTGTAGATTAT 60
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Job time : 2776.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:18:04 ; Search time 2274.9 seconds
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7652.923 Million cell updates/sec

Title: US-09-155-327G-6

Perfect score: 583
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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27: em_gss_vrl:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 522.8 | 89.7 | 582 | AY421022 | AY421022 Mus muscu |

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| 6 | 522.8 | 89.7 | 3487 | 11 | AK004680 | AK004680 Mus muscu |
| 7 | 521.2 | 89.4 | 969 | 12 | BY715200 | BY715200 BY715200 |
| 8 | 483.4 | 82.9 | 697 | 12 | BT770566 | BT770566 603060362 |
| 9 | 465.6 | 79.9 | 967 | 13 | BUS03850 | BUS03850 AGENCOURT |
| 10 | 443 | 76.0 | 626 | 14 | CA391923 | CA391923 C820C09.Y |
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| 16 | 360 | 61.7 | 548 | 14 | CA407839 | CA407839 1004048.H |
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| 25 | 305.2 | 52.3 | 559 | 13 | CF533813 | CF533813 UI-M-FY0- |
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| 36 | 254.4 | 44.2 | 430 | 14 | CB760687 | CB760687 AMGNMUC:N |
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ALIGNMENTS

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DEFINITION Homo sapiens BC1212 gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION AY421020
VERSION AY421020.1 GI:39776977
KEYWORDS
SOURCE GSS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,D.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarwal,A., Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,D.J., Adams,M.D. and Cargill,M.
Direct Submission
TITLE

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

Source

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ORIGIN

Query Match 98.2%; Score 572.4; DB 29; Length 582;
Best Local Similarity 99.0%; Pred. No. 1.5e-120;
Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 121 CCGCTGACACCAAGCAGCTGCGGCGAGTGAAGTGTGAGACCCGCTTCCGCGCACC 180
QY 181 TTCTCTGATCTGGGCGCTCAGCTGATGATGACCCAGGCTCAGCCCAAGACGCTTACC 240
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DB 481 CGTCTGCGGAGAGGGAACCTGAGCACTGAGTGAAGCAAGTGTGACGCGGGGCTGTGGCACTG 540
QY 541 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTCTGAGCAAGTGA 582
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RESULT 2 AL157542 804 bp mRNA linear EST 04-SEP-2003

LOCUS DKEF2761D0816.r1 761 (synonym: hamy2) Homo sapiens cDNA clone

DEFINITION DKEF2761D0816 5', mRNA sequence.

ACCESSION AL157542 GI:7057943

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 804)

Authors Ansoerge, W., Wilkner, U., Mewes, W., Weil, B. and Wiemann, S.

TITLE EST (Ansoerge, W., Wilkner, U., Mewes, W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)

CONTACT MIPs

INGOLSTADTER Landstr. 1, D-85764 Neuberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;

Sequenced by EMBL (European Molecular Biology Laboratories,

Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No sequence available.

This clone (DKEF2761D0816) is available at the RZPD in Berlin.

Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

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/tissue_type="amygdala"
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/lab_host="MD10B"
/clone_lib="761 (synonym: hamy2)"
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ORIGIN

Query Match 94.3%; Score 550; DB 9; Length 804;
Best Local Similarity 96.6%; Pred. No. 2.3e-115;
Matches 575; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY 1 ATGGGACCCGAGCTTGGCCGACACACACGCGGCTTGTGTGACAGACTTTGAGTTAT 60
DB 1 ATGGGACCCGAGCTTGGCCGACACACACGCGGCTTGTGTGACAGACTTTGAGTTAT 60
QY 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTTGGCCCGGAGAGGCCCAAGACTGAC 120
DB 61 AAGCTGAGGCGAAGAGGTTATGTCTGTGAGCTTGGCCCGGAGAGGCCCAAGACTGAC 120
QY 121 CCGCTGACACCAAGCAGCTGCGGCGAGTGAAGTGTGAGACCCGCTTCCGCGCACC 180
DB 121 CCGCTGACACCAAGCAGCTGCGGCGAGTGAAGTGTGAGACCCGCTTCCGCGCACC 180
QY 181 TTCTCTGATCTGGGCGCTCAGCTGATGATGACCCAGGCTCAGCCCAAGACGCTTACC 240
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DB 241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAATGSGGCGGCTTGTAGCTTTCTT 300
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QY 361 CAATGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAATGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AGTGGGGGCTGGGCGGAGTTCAAGCTTATACCGGGGACCGGGGCTTGAAGAGCGCGG 480
DB 421 AGTGGGGGCTGGGCGGAGTTCAAGCTTATACCGGGGACCGGGGCTTGAAGAGCGCGG 480
QY 481 CGTCTGCGGAGAGGGAACCTGAGCACTGAGTGAAGCAAGTGTGACGCGGGGCTGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGAACCTGAGCACTGAGTGAAGCAAGTGTGACGCGGGGCTGTGGCACTG 540
QY 541 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTCTGAGCAAGTGA 583
DB 541 GGGGCGCTGTGTAAGTGTGAGGGGCTTTTCTGAGCAAGTGA 583

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RESULT 3
BE793530      1030 bp      mRNA      linear      EST 20-SEP-2000
LOCUS         601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
DEFINITION    mRNA sequence.
ACCESSION     BE793530
VERSION       BE793530.1 GI:10214832
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1030)
              NIH-MGC http://mgc.nci.nih.gov/,
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              Tissue Procurement: DCTD/DTF
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
              Plate: LHC800 row: p column: 04
              High quality sequence start: 5
              High quality sequence stop: 709.
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               insert size 1.8kb. Library constructed by Ling Hong in
               the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Query Match 94.1%; Score 548.4; DB 10; Length 1030;
Best Local Similarity 96.4%; Pred. No. 66-115;
Matches 561; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

1 ATGGCGACCCCAAGCTTGGCGCCCAAGACACAGGAGCTTGTGTCAGACTTTGAGGTAT 60
144 ATGGCGACCCCAAGCTTGGCGCCCAAGACACAGGAGCTTGTGTCAGACTTTGAGGTAT 203
61 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGCTGGCCCGGGAGGAGGAGGAGGAGGAGG 120
204 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGCTGGCCCGGGAGGAGGAGGAGGAGGAGG 263
121 CCGGTGACCAAGCAATGCGGAGCTGAGATGATGATGACACCGGCTTCGGGCGAC 180
264 CCACTGCACCAAGCAATGCGGAGCTGAGATGATGATGACACCGGCTTCGGGCGAC 323
DB 181 TTCTGTATCTGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 324 TTCTGTATCTGGCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 383
QY 241 CAGGCTTCGACGAACTTTTCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 384 CAGGCTTCGACGAACTTTTCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443
QY 301 CTCTTGGGGGTGACGTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATG 360

DB 444 GTCTTTGGGGGTGACGTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATG 503
QY 361 CAACTGCACCAAGCAATGCGGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 504 CAACTGCACCAAGCAATGCGGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 563
QY 421 AGTGGAG 480
DB 564 AGTGGAG 623
QY 481 CGTGTGCGGAG 540
DB 624 CGTGTGCGGAG 683
QY 541 GGGGCGCTGTAACTGTAGAG 582
DB 684 GGGGCGCTGTAACTGTAGAG 725

RESULT 4
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LOCUS Mus musculus BCL2L2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY421022
VERSION AY421022.1 GI:39776979
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 582)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Ciavella,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
JOURNAL 14671302
PUBMED
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Ciavella,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
 based on alignment.
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ORIGIN

Query Match 89.7%; Score 522.8; DB 29; Length 582;
Best Local Similarity 93.6%; Pred. No. 3.4e-109;
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

1 ATGGGACCCCAAGCTTGGCGCCCAAGACACAGGAGCTTGTGTCAGACTTTGAGGTAT 60
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QY 61 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGCTGGCCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
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| Db | | 121 | CCGCTGCACCAAGCCATCGGGGTGCTGGAGACGAAGTTTGAAGCCGTTTCGCCCGCACC | 180 |
| QY | | 181 | TTCTTGATGTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCACGACAAGCTTCACC | 240 |
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| QY | | 241 | CAGGTCCTCCAGCACACTTTTTCAGAAGGGGGCCCCAATCGGGGCGCGCCCTTAGAGCTTTT | 300 |
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| QY | | 361 | CAAATGACAGAGTGAATGATGGGCTTACCTGGAGACGCGGCTGTGACTGATCCACAGC | 420 |
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| Db | | 421 | AGTGGGGGCTTGGCGGAGTTTACAGCTCTTAAACGGGGACGGGGCCCTTGAGAGGACGCG | 480 |
| QY | | 481 | CGTGTGGGGAGGGGAACTGGGCGATCAGTAGAGACAGTGTGACGGGGGCGGTGGCACTG | 540 |
| Db | | 481 | CGTGTGGGGAGGGGAACTGGGCGATCAGTAGAGACAGTGTGACGGGGGCGGTGGCACTG | 540 |
| QY | | 541 | GGGGCCCTGTGTAATCTGTAGGGGCTTTTGTGCTAGCAAGTGA | 582 |
| Db | | 541 | GGGGCCCTGTGTAATCTGTAGGGGCTTTTGTGCTAGCAAGTGA | 582 |
| RESULT 5 | | | | |
| AKO15644 | | | | |
| LOCUS | | | | |
| DEFINITION | | | | |
| AKO15644 | | 1949 bp | mRNA | linear HTC 20-SEP-2003 |
| DESCRIPTION | | | | Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048B08 Product:Bcl2-like 2, full insert sequence. |
| ACCESSION | | | | |
| VERSION | | | | AKO15644.1 GI:12854052 |
| KEYWORDS | | | | HTC; CAP trapper. |
| SOURCE | | | | Mus musculus (house mouse) |
| ORGANISM | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| REFERENCE | | | | |
| AUTHORS | | 1 | Carninci, P. and Hayashizaki, Y. | |
| TITLE | | | High-efficiency full-length cDNA cloning | |
| JOURNAL | | | Meth. Enzymol. 303, 19-44 (1999) | |
| MEDLINE | | | 99279253 | |
| PUBMED | | | 10349626 | |
| REFERENCE | | 2 | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | |
| AUTHORS | | | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | |
| TITLE | | | Genome Res. 10 (10), 1617-1630 (2000) | |
| JOURNAL | | | 20499374 | |
| MEDLINE | | | 11042159 | |
| PUBMED | | | 3 | |
| REFERENCE | | | | |
| AUTHORS | | | Shibata, K., Itoh, M., Azawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitsuma, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Isikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawat, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. | |
| TITLE | | | RIKEN integrated sequence analysis (RISA) system--384-Format sequencing pipeline with 384 multicapillary sequencer | |
| JOURNAL | | | Genome Res. 10 (11), 1757-1771 (2000) | |
| MEDLINE | | | 20530913 | |
| PUBMED | | | 11076861 | |
| REFERENCE | | 4 | | |

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AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
TITLE        Functional annotation of a full-length mouse cDNA collection  
JOURNAL      Nature 409, 685-690 (2001)  
REFERENCE    5  
AUTHORS      The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II team.  
TITLE        Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL      Nature 420, 563-573 (2002)  
REFERENCE    6 (bases 1 to 1949)  
AUTHORS      Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arono,H.,  
Arikawa,T., Bono,H., Caminici,P., Fukuda,S., Fukushima,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
Kasukabe,T., Kato,C., Kawai,J., Kojima,Y., Komoh,H., Koude,M.,  
Koys,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K., Nunazaki,R., Ohno,M., Okazaki,Y., Okioto,T., Owa,C.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suizuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,T., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
TITLE        Direct SubMISSION  
JOURNAL      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,  
Kanagawa 220-0045, Japan (E-mail:genome-resgsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
COMMENT      please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details  
CDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
15' GAGCAGACGAGCATCCAGACGCCTTTTATTTTATTVN 3'). cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequence 15'  
GAGCAGACGATTCGAGTAATTAAATAAACCCCCCCCCCCC 3'. cDNA was cleaved  
with BamHI and XhoI. cDNA of size compised longer than 7 kb was  
selected before cloning. Vector: a modified pluescript KS(+) after  
bulk excision from lambda FLC I. Cloning sites, 5' end: SalI; 3'  
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Query Match      89.7%; Score 522.8; DB 11; Length 3487;
Best Local Similarity 93.6%; Pred. No. 7.6e-109;
Matches 545; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 1 ATGGGACCCCAAGCTTGGGCCCCGAGACACCGGGCTGTGGTGAGAGACTTTGATGTTAT 60
DB 209 ATGGGACCCCAAGCTTGGGCCCCGAGACACCGGGCTGTGGTGAGAGACTTTGATGTTAT 268
QY 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGAGAGGCCCCAGAGAGCTGAC 120
DB 269 AAGCTGAGGAGAGAGGTTATGTCTGTGAGAGCTGGCCCCGAGAGGCCCCAGAGAGCTGAC 328
QY 121 CCGCTGACCAAGCCATGCGGCGAGAGCTGAGAGATGTTGACAGACCGGCTTCCGCGCACC 180
DB 329 CCGCTGACCAAGCCATGCGGCGAGAGCTGAGAGATGTTGACAGACCGGCTTCCGCGCACC 388
QY 181 TTCTTGTATCTGGGCGCTCAGCTGATGTGACCCCAAGGCTTCAAGCCAGCAAGCTTTAC 240
DB 389 TTCTTGTATCTGGGCGCTCAGCTGATGTGACCCCAAGGCTTCAAGCCAGCAAGCTTTAC 448
QY 241 CAGGCTCCGAGAGAACTTTTCAAGGGGGCCCCCAACTGGGGCGGCTTGTAGCTTTCTT 300
DB 449 CAGGCTCCGAGAGAACTTTTCAAGGGGGCCCCCAACTGGGGCGGCTTGTAGCTTTCTT 508
QY 301 CTCTTTGGGGGCTGCACTGTGTGTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
DB 509 GTCTTTGGGGGCTGCGCTGTGTGTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 568
QY 361 CAACTGACAGAGTGTGATGTGTGCTTACTCTGAGAGCGGCGCTGTGACTGTGATCAAGC 420
DB 569 CAACTGACAGAGTGTGATGTGTGCTTACTCTGAGAGCGGCGCTGTGACTGTGATCAAGC 628
QY 421 AGTGGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGGAGCGGGCGGCTTGTGAGAGAGCGCGG 480
DB 629 AGTGGGGGCTGGGCGGAGTTTCAACAGCTTATACGGGGAGCGGGCGGCTTGTGAGAGAGCGCGG 688
QY 481 CGTTCGCGGAGAGGAGACTGGGCGATCAGTGAAGACAGTGTGACGCGGGCGGCTTGTGAGAGAGCGG 540
DB 689 CGTTCGCGGAGAGGAGACTGGGCGATCAGTGAAGACAGTGTGACGCGGGCGGCTTGTGAGAGAGCGG 748
QY 541 GGGGCGCTGTGACTGTGAGAGGCGCTTTTGTGTACCAAGTGA 582
DB 749 GGGGCGCTGTGACTGTGAGAGGCGCTTTTGTGTACCAAGTGA 790

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RESULT 7
BY715200          969 bp      mRNA      linear      EST 17-DEC-2002
LOCUS             BY715200      full-length enriched, adult male testis Mus musculus
DEFINITION        CDNA clone 4930468D08 5', mRNA sequence.
ACCESSION         BY715200
VERSION           BY715200.1 GI:27128317
KEYWORDS
SOURCE            Mus musculus (house mouse)
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 969)

```

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nixaido, I., Oseto, N., Saito, R., Suzuki, H., Yamana, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, I., Matsuda, H., Batelov, S., Beisel, K. W., Blake, J. A., Brack, D., Brusic, V., Chochia, C., Corbani, L. E., Coumans, S., Daille, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gless, C., Godzik, A., Gough, J., Grimmond, S., Guerino, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sander, A., Schneider, C., Sempole, C. A., Setou, M., Shimada, K., Sulciner, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imoto, K., Ichi, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

MEDLINE

22354683

PUBMED

1246851

COMMENT

Contact: Yoshihide Hayashizaki
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1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashizaki, K., Hirozane, T., Hori, F., Imoto, K., Ichi, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, N., Nomura, K., Nunazaki, R., Ohno, M., Oseto, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

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1..969
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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DB 565 GCAGTGGGGGCTGGCGGAGATTCAACAGCTTATACGGGGGACGGGGCCCTTGAGAGAGGCG 624
QY 478 CGGCGTCTGGGAGAGGGGGAAGCTGGGGA-TCAGTGAAGACAG-TGCTGACGGGGGCGCTGG 535
DB 625 CGGGGTCTCGGGAGGGGGAAGCTGGGCACTCAGTGAAGACAGTTGCTGACGGGAGCCGTGG 684
QY 536 CACTGGGGGCGCT 548
DB 685 CACTGGGGGCGCT 697

RESULT 9
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LOCUS AGENCOURT_10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
DEFINITION 5', mRNA sequence.
ACCESSION BUS03850
VERSION BUS03850.1 GI:22810083
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 967)
TITLE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L14M1403 row: C column: 23
High quality sequence stop: 524.
Location/Qualifiers
1..967
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/db_xref="taxon:10090"
/clone="IMAGE:6491566"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 79.9%; Score 465.6; DB 13; Length 967;
Best Local Similarity 92.5%; Pred. No. 5; 4e-96;
Matches 544; Conservative 0; Mismatches 39; Indels 5; Gaps 5;

QY 1 ATGGGAGACCCCGGCTGGCGGAGACACAGGGGCTGGGGAGAGATTGTAGGTTAT 60
DB 130 ATGGGAGACCCCGGCTGGCGGAGACACAGGGGCTGGGGAGAGATTGTAGGTTAT 189
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGCCCGGGAGAGGCCACAGAGCTGAC 120
DB 190 AAGCTGAGGACAGAGGTTATGTCTGTGAGAGTGGCCCGGGAGAGGCCACAGAGCTGAC 249
QY 121 CGGCTGACCAAGCAATGGGGGAGAGTGAAGTTCGAGACCCGCTTCCGGGACACC 180
DB 250 CGGCTGACCAAGCAATGGGGGAGAGTGAAGTTCGAGACCCGCTTCCGGGACACC 309

QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGATGCCAGGCTTCAGCCAGCAAGCTTCACC 240
DB 310 TTCTCTGATCTGGCGGCTCAGCTGCATGTGATGCCAGGCTTCAGCCAGCAAGCTTCACC 369
QY 241 CAGGCTTCGACGAACTTTTTCAGAGGGGGCCCACTGGGGGCGCCCTTGTAGCCTTCTT 300
DB 370 CAGGCTTCGACGAACTTTTTCAGAGGGGGCCCTTACAGGGGCGCCCTTGTAGCCTTCTT 429
QY 301 CTTCTTGGGGGCTGCAGCTGTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGGTGGGA 360
DB 430 GTCTTTGGGGGCTGCAGCTGTGCTGAGAGTGTCAACAAGAGATGAGAACCACTGGTGGGA 489
QY 361 CAAGTCAGAGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 419
DB 490 CAAGTCAGAGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 549
QY 420 CAGT-GGGGAGTGGGCGGAGTTCAAGAGTCTTAAACGGGGAC-GGGGCGCTGGAGAGGCG 477
DB 550 CAGTGGGGGCTGGGCGGAGTTCAAGAGTCTTAAACGGGGACGGGGCGCTGGAGAGGCA 609
QY 478 CGGCTCTCGCGGAGGGGAACTGGGCACTGAGTGAAGACAGTGTGAC-GGGGCGCTGGG 536
DB 610 CGGCTCTCGCGGAGGGGAACTGGGCACTGAGTGAAGACAGTGTGACGGGGGCGCTGGG 669
QY 537 ACTGGGGGCGCTGGGAACTGT-AGGGGCGCTTTTGTGAGCAAGTGAA 583
DB 670 ACTGGGGGCGCTGGGAACTGT-AGGGGCGCTTTTGTGAGCAAGTGAA 717

RESULT 10
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LOCUS cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA cs20c09
DEFINITION (un-normalized, unambigified): cs Homo sapiens cDNA clone
5', mRNA sequence.
ACCESSION CA391923
VERSION CA391923.1 GI:24724221
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS Wislow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPE/choroid for the
NIH Bank Project: Over 600 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
JOURNAL MEDLINE 22107410
PUBMED 12107410
COMMENT Contact: Wislow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 20 row: C column: 09
Seq primer: M13R1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="RPE/choroid"
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/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(un-normalized, unambigified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of

ORIGIN

dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>. The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mui sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

Query Match 76.0%; Score 443; DB 14; Length 626;
Best Local Similarity 98.7%; Pred. No. 6,6e-91;
Matches 446; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTTGGCCCGACACACAGGGCTCTGGTGCAGACTTTGTAGTTAT 60
DB 175 ATGGCGACCCCGAGCTTGGCCCGACACACAGGGCTCTGGTGCAGACTTTGTAGTTAT 234
QY 61 AACCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCACAGCTGAC 120
DB 235 AACCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCACAGCTGAC 294
QY 121 CCGCTGACCAAGCCATGCGGGAGCGAGATGAGTGGAGACCCGCTTCCGGCGCACC 180
DB 295 CCGCTGACCAAGCCATGCGGGAGCGAGATGAGTGGAGACCCGCTTCCGGCGCACC 354
QY 181 TTCTGTGATCTGCGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAAGCTTCAAC 240
DB 355 TTCTGTGATCTGCGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAAGCTTCAAC 414
QY 241 CAGGCTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCTTTCTT 300
DB 415 CAGGCTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCTTTCTT 474
QY 301 CTCTTTGGGGCTGACCTGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGAT 360
DB 475 GTCTTTGGGGCTGACCTGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGAT 534
QY 361 CAGGTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 535 CAGGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
QY 421 AGTGGGGGCTGGCGGAGTTCAAGCTCTATA 452
DB 595 AGTGGGGGCTGGCGGAGTTCAAGCTCTATA 626

RESULT 11
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LOCUS 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
DEFINITION mRNA sequence.
ACCESSION BI910270
VERSION BI910270.1 GI:16173653
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 643)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M11548 row: j column: 23
High quality sequence stop: 643.
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/mol_type="mRNA"
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/note="Vector: pCMV-SPORT6, site 1: NotI, site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC library."

ORIGIN

Query Match 71.6%; Score 417.6; DB 12; Length 643;
Best Local Similarity 93.7%; Pred. No. 4,4e-85;
Matches 446; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 1 ATGGCGACCCCGAGCTTGGCCCGACACACAGGGCTCTGGTGCAGACTTTGTAGTTAT 60
DB 140 ATGGCGACCCCGAGCTTGGCCCGACACACAGGGCTCTGGTGCAGACTTTGTAGTTAT 199
QY 61 AACCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCACAGCTGAC 120
DB 200 AACCTGAGGAGAGAGGTTATGTCTGTGAGCTGGCCCGGAGAGGCCACAGCTGAC 259
QY 121 CCGCTGACCAAGCCATGCGGGAGCGAGATGAGTGGAGACCCGCTTCCGGCGCACC 180
DB 260 CCGCTGACCAAGCCATGCGGGAGCGAGATGAGTGGAGACCCGCTTCCGGCGCACC 319
QY 181 TTCTGTGATCTGCGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAAGCTTCAAC 240
DB 320 TTCTGTGATCTGCGGCTCAGCTGATGATGACCCCGAGCTCAGCCAGCAAGCTTCAAC 379
QY 241 CAGGCTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCTTTCTT 300
DB 380 CAGGCTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCTTTCTT 439
QY 301 CTCTTTGGGGCTGACCTGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGAT 359
DB 440 GTCTTTGGGGCTGACCTGTGTGCTGAGATGATGATGATGATGATGATGATGATGATGAT 499
QY 360 ACAAGTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
DB 500 ACAAGTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 559
QY 420 CAGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGGAGCGGGCCCTGAGAGAGG 475
DB 560 CAGTGGGGGCTGGCGGAGTTCAAGCTCTATAAGGGAGCGGGCCCTGAGAGAGG 615

RESULT 12
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LOCUS 602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
DEFINITION 5', mRNA sequence.
ACCESSION BF785386
VERSION BF785386.1 GI:12090422
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 815)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LHM9853 row: h column: 07
High quality sequence start: 3
High quality sequence stop: 650.

FEATURES

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/clone_lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library." Location/Qualifiers

ORIGIN

Query Match 68.1%; Score 397; DB 10; Length 815;
Best Local Similarity 91.1%; Pred. No. 2.6e-80;
Matches 500; Conservative 0; Mismatches 40; Indels 9; Gaps 7;
21 CCCAGACACACGGGCTGTGTGAGAGATTGATTAAGCTGAGGACGAGGTTA 80
2 CCCAGACACACGGGCTGTGTGAGAGATTGATTAAGCTGAGGACGAGGTTA 60
81 TGTCTGTGAGAGCTGGCCCGGGGAGAGGCCAGAGCTGAGCCGCTGACACCAAGCATGCG 140
61 TGTCTGTGAGAGCTGGCCCGGGGAGAGGCCAGAGCTGAGCCGCTGACACCAAGCATGCG 120
141 GGCAGCTGAGAGTGAATTCAGAGACCCGCTTCCGGGAGCATTCTCTGATCTGGGGGTCA 200
121 GGCCTGTGAGAGCGAGTT-GAGACCCGCTTCCGGGAGCATTCTCTGATCTGGGGGTCA 179
201 GGTGATGTGACCCAGGCTGAGCCAGACAGCTTCAACCAGGTTCCGACGAATTTT 260
180 GGTACACGAGACCCAGGCTGAGCCAGACAGCTTCAACCAGGTTCCGACGAATTTT 239
261 TCAGAGGGGCCCCAAGCTGGGGCCGCTTGAAGCTTCTTCTCTTGGGGGTGACATGTG 320
240 CCAAGGGGGCCCTAAGCTGGGGCCGCTTGTGGCATTC---TGTCTGGGGGTGCTGTG 296
321 TGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGTGTGGAACAAGTGCAGAGTGAATGT 380
297 TGTCTGAGAGTGTCAACAAAGAGATGAAACCACTGTGTGGAACAAGTGCAGAGTGAATGT 355
381 GGCCTTACCTGAGAGACGGCGCTGTGATCGATCCACAGCAGTGGGGGTGAGGAGTT 440
356 GGCCTTACCTGAGAGACGGCGCTGTGATCGATCCACAGCAGTGGGGGTGAGGAGTT 415
441 CACAGCTTATACGGGGAACGGGGCCCTGAGAGAGGCGGCGTCTGCGGAGAGGAACTG 500
416 CACAGCTTATACGGGGAACGGGGCCCTGAGAGAGGCGGCGTCTGCGGAGAGGAACTG 473
501 GGCATCAGTGAAGACAGTGTCTGACGAGGGGCGTGCACATGGGGGCGCTGTGATCTGTGG 560
474 GGCATCAGTGAAGACAGTGTCTGACGAGGGGCGTGCACATGGGGGCGCTGTGATCTGTGG 532
561 GGCCTTTT 569
|||||

Db 533 GGCCTTTT 541

RESULT 13
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LOCUS
DEFINITION CB578463 623 bp mRNA linear EST 03-APR-2003
AMGN:NCI:RNDG1-00100-H10-A nrdg1 (10855) Rattus norvegicus CDNA
clone nrdg1-00100-h10 5', mRNA sequence.
ACCESSION CB578463
VERSION CB578463.1 GI:29522504
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
Rattus.
1..623
Location/Qualifiers

FEATURES

source

1..623
/organism="Rattus norvegicus"
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/clone="nrdg1-00100-h10"
/tissue_type="Dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat dorsal root ganglia" Location/Qualifiers

ORIGIN

Query Match 65.5%; Score 381.8; DB 14; Length 623;
Best Local Similarity 92.6%; Pred. No. 6.9e-77;
Matches 401; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
1 ATGGGACCCCAAGCCTCGGCCCAACACACAGGAGCTGTGTGAGAGCTTTAGATTAT 60
191 ATGGGACCCCAAGCCTCGGCCCAACACACAGGAGCTGTGTGAGAGCTTTAGATTAT 250
61 AAGCTGAGGACAAAGGTTATGTCTGTGAGAGCTGGCCCGGGGAGGAGGCCAGACTGAC 120
251 AAGCTGAGGACAAAGGTTATGTCTGTGAGAGCTGGCCCGGGGAGGAGGCCAGACTGAC 310
121 CCGCTGACCAAGACCAATGCGGAGCTGAGATGAGTTGAGACCCGCTTCCGGGCGACC 180
311 CCGCTGACCAAGACCAATGCGGAGCTGAGATGAGTTGAGACCCGCTTCCGGGCGACC 370
181 TTCTCTGATCTGCGGCTCAGCTGATGATGACCCCAAGCTCAGCCCAAGAGCTTTCACC 240
371 TTCTCTGATCTGCGGCTCAGCTGATGATGACCCCAAGCTCAGCCCAAGAGCTTTCACC 430
241 CAGGCTCCGACGAATTTTTCAGAGGGGGCCCCAAGTGGGGCGGCTTGTAGCTTTCT 300
431 CAGGTTCCGACGAATTTTTCAGAGGGGGCCCCAAGTGGGGCGGCTTGTAGCTTTCT 490
301 CTCTTTGGGGCTGACATGTGTGTGAGATGATCAACAAGAGATGAAACCACTGTGGGA 360
491 GTCTTTGGGGCTGACATGTGTGTGAGATGATCAACAAGAGATGAAACCACTGTGGGA 550
361 CAAAGTCAGAGATGATGTGTGCTTACCTGAGACCGGCGCTGTGATCCAGAC 420
551 CAAAGTCAGAGATGATGTGTGCTTACCTGAGACCGGCGCTGTGATCCAGAC 610
421 AGTGGGGGCTGGG 433
611 AGTGGGGGCTGGG 623
|||||

| RESULT 14 | AK013244 | 554 bp | mRNA | linear | HTC 20-SEP-2003 |
|------------|---|-------------|------|--------|-----------------|
| LOCUS | AK013244 | | | | |
| DEFINITION | Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810455A13 product:Bcl2-like 2, full insert sequence. | | | | |
| ACCESSION | AK013244 | | | | |
| VERSION | AK013244.1 | GI:12650487 | | | |
| KEYWORDS | HTC; CAP trapper. | | | | |
| SOURCE | Mus musculus (house mouse) | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. | | | | |
| REFERENCE | Carninci, P. and Hayashizaki, Y. | | | | |
| AUTHORS | 1 | | | | |
| TITLE | High-efficiency full-length cDNA cloning | | | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | | | |
| MEDLINE | 99279253 | | | | |
| PUBMED | 10349636 | | | | |
| REFERENCE | 2 | | | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | | | | |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | | | |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | | | | |
| MEDLINE | 20499374 | | | | |
| PUBMED | 11042159 | | | | |
| REFERENCE | 3 | | | | |
| AUTHORS | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitsumaki, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | | | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer | | | | |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) | | | | |
| MEDLINE | 20530913 | | | | |
| PUBMED | 11076861 | | | | |
| REFERENCE | 4 | | | | |
| AUTHORS | The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | | | | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | | | |
| JOURNAL | Nature 409, 685-690 (2001) | | | | |
| MEDLINE | | | | | |
| PUBMED | | | | | |
| REFERENCE | 5 | | | | |
| AUTHORS | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | | | | |
| TITLE | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs | | | | |
| JOURNAL | Nature 420, 563-573 (2002) | | | | |
| MEDLINE | 6 (bases 1 to 854) | | | | |
| PUBMED | | | | | |
| REFERENCE | 6 | | | | |
| AUTHORS | Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaitakawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, C., M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takaheishi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamatsu, M. and Hayashizaki, Y. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suhei-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-reasegc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216] | | | | |

[illegible]

immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 7,3e-136;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTGTGGTGGAGACTTTGTAGTTAT 60
DB 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTGTGGTGGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCCGAGAGCTGAC 120
DB 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCCGAGAGCTGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
DB 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCAGGCTTCAAGCCAGCAAGCTTACC 240
DB 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCAGGCTTCAAGCCAGCAAGCTTACC 240
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
DB 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
DB 301 CTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTGCAGAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGATGATCAACAGC 420
DB 361 CAAGTGCAGAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGATGATCAACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTCACAGCTCTAATCGGGGAGCGGGCCCTTGGAGAGGCGCG 480
DB 421 AGTGGGGGCTGGGGGAGTTCACAGCTCTAATCGGGGAGCGGGCCCTTGGAGAGGCGCG 480
QY 481 CGTCTGCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGCGGGCCGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGCGGGCCGTGGCACTG 540
QY 541 GGGGGCCCTGGTACTGTAGAGGGGCTTTTGTAGCAAGTAGAA 583
DB 541 GGGGGCCCTGGTACTGTAGAGGGGCTTTTGTAGCAAGTAGAA 583

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RESULT 2
AA25134
ID AAX25134 standard; DNA; 583 BP.

AA25134;
05-JUL-1999 (first entry)
Human bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
animal model; ss.
Homo sapiens.
MO913710-A1.
25-MAR-1999.

16-SEP-1998; 98WO-AU000764.
16-SEP-1997; 97AU-00009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Cory S, Adams J, Print C, Gibson L, Koentgen F;

WPI; 1999-243690/20.
P-PSDB; AA05532.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AA05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 583; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 7,3e-136;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTGTGGTGGAGACTTTGTAGTTAT 60
DB 1 ATGGGAGCCCGAGCTGGGCCCCGAGACACAGGGGCTGTGGTGGAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCCGAGAGCTGAC 120
DB 61 AAGCTGAGGACAGAGGTTATGTCTGTGAGCTGGCCCCGGGAGAGGCCCGAGAGCTGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
DB 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATAGATTGAGACCCGCTTCCGGCGAC 180
QY 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCAGGCTTCAAGCCAGCAAGCTTACC 240
DB 181 TTCTCTGATCTGGCGGCTCACTGATGATGACCCAGGCTTCAAGCCAGCAAGCTTACC 240
QY 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
DB 241 CAGGTCTCCGACGAATTTTCAAGGGGGGCCCAACTGGGGCCGCTTGTAGCTTCTTT 300
QY 301 CTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
DB 301 CTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAGAGATGGAACCACTGGTGGGA 360
QY 361 CAAGTGCAGAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGATGATCAACAGC 420
DB 361 CAAGTGCAGAGAGTGTGATGTGGCTTACCTGAGACGCGGCTGTGATGATCAACAGC 420
QY 421 AGTGGGGGCTGGGGGAGTTCACAGCTCTAATCGGGGAGCGGGCCCTTGGAGAGGCGCG 480
DB 421 AGTGGGGGCTGGGGGAGTTCACAGCTCTAATCGGGGAGCGGGCCCTTGGAGAGGCGCG 480
QY 481 CGTCTGCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGCGGGCCGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGGAACCTGGGCATCAGTGAAGACAGTGTGACGCGGGCCGTGGCACTG 540

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CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by plasmid/viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
CC
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGGACCCCGAGCTTGGCCCGACACACAGGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 1 ATGGGACCCCGAGCTTGGCCCGACACACAGGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGCCCGGAGAGGCGCCAGAGCTGAC 120
DB 61 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGCCCGGAGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACACAGCCATGCGGCGAGCTGAGATGATGAGACCCGCTTCGGCGGAC 180
DB 121 CCGCTGACACAGCCATGCGGCGAGCTGAGATGATGAGACCCGCTTCGGCGGAC 180
QY 181 TTCTTGATCTGGCGGCTGAGCTGATGTACCCAGGCTAGCCAGCAAGCTTCAAC 240
DB 181 TTCTTGATCTGGCGGCTGAGCTGATGTACCCAGGCTAGCCAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGGCCCAACTGGGGGCCGCTTGATGCTT 300
DB 241 CAGGCTCCGACGAACTTTTCAAGGGGGGCCCAACTGGGGGCCGCTTGATGCTT 300
QY 301 CTCTTTGGGGCTGACCTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
DB 301 CTCTTTGGGGCTGACCTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
QY 361 CAAGTGAAGAGTGTGATGATGCTTACCTGAGACGCGGCTGTGATGATCAAC 420
DB 361 CAAGTGAAGAGTGTGATGATGCTTACCTGAGACGCGGCTGTGATGATCAAC 420
QY 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGGAAGGGGCCCTGGAAGAGCGCG 480
DB 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGGAAGGGGCCCTGGAAGAGCGCG 480
QY 481 CGCTGACCAAGCCATGCGGCGAGCTGAGATGAGAGCAAGTGTGACGGGGGCCGCTG 540
DB 481 CGCTGACCAAGCCATGCGGCGAGCTGAGATGAGAGCAAGTGTGACGGGGGCCGCTG 540
QY 541 GGGGCGCTGTGATGATGAGAGGCTTTTGTGTAACAAGTA 582
DB 541 GGGGCGCTGTGATGATGAGAGGCTTTTGTGTAACAAGTA 582
```

RESULT 5
ABX09972
ID ABX09972 standard; DNA; 582 BP.

XX 23-JAN-2003 (first entry)
XX Human bcl-w DNA fragment SEQ ID 37.
XX
XX
XX Oligonucleotide; interferon; oncogene; cytokine; id; developmental;
XX prion; inhibition; human; de.
XX Homo sapiens.
XX
XX
XX DE10100587-C1.

XX 21-NOV-2002.
XX
XX 09-JAN-2001; 2001DE-01000587.
XX
XX 09-JAN-2001; 2001DE-01000587.
XX
XX (R100-) R100PHARMA AG.
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-742209/81.
XX
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
XX PT introduction of complementary double-stranded oligonucleotide, after
XX PT treating the cell with interferon.
XX
XX Disclosure; Page 35-36; 98pp; German.

CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the target gene at
CC least one oligonucleotide (dsRNA) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with
CC the target gene and the cells are treated with interferon before
CC introduction of dsRNA. The method is used to inhibit expression of
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)
CC protein genes; developmental or prion genes; or genes expressed in
CC pathogenic organisms (particularly plasmids) or in viruses or viroids
CC (pathogenic in humans, animals or plants). Treating the cells with
CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC are modified to increase their stability. ABX09936-ABX10075 represent
CC gene fragments used to illustrate the method of the invention

SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 99.0%; Score 577.2; DB 6; Length 582;
Best Local Similarity 99.5%; Pred. No. 2e-134;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGGACCCCGAGCTTGGCCCGACACACAGGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
DB 1 ATGGGACCCCGAGCTTGGCCCGACACACAGGGGCTCTGGTGGCAGACTTTGTAGTTAT 60
QY 61 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGCCCGGAGAGGCGCCAGAGCTGAC 120
DB 61 AAGCTGAGGACGAGAGGTTATGCTGTGAGCTGGCCCGGAGAGGCGCCAGAGCTGAC 120
QY 121 CCGCTGACACAGCCATGCGGCGAGCTGAGATGATGAGACCCGCTTCGGCGGAC 180
DB 121 CCGCTGACACAGCCATGCGGCGAGCTGAGATGATGAGACCCGCTTCGGCGGAC 180
QY 181 TTCTTGATCTGGCGGCTGAGCTGATGTACCCAGGCTAGCCAGCAAGCTTCAAC 240
DB 181 TTCTTGATCTGGCGGCTGAGCTGATGTACCCAGGCTAGCCAGCAAGCTTCAAC 240
QY 241 CAGGCTCCGACGAACTTTTCAAGGGGGGCCCAACTGGGGGCCGCTTGATGCTT 300
DB 241 CAGGCTCCGACGAACTTTTCAAGGGGGGCCCAACTGGGGGCCGCTTGATGCTT 300
QY 301 CTCTTTGGGGCTGACCTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
DB 301 CTCTTTGGGGCTGACCTGTGCTGAGAGTGTCAACAGAGATGAAACCACTGATGGA 360
QY 361 CAAGTGAAGAGTGTGATGATGCTTACCTGAGACGCGGCTGTGATGATCAAC 420
DB 361 CAAGTGAAGAGTGTGATGATGCTTACCTGAGACGCGGCTGTGATGATCAAC 420
QY 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGGAAGGGGCCCTGGAAGAGCGCG 480
DB 421 AGTGGGGGCTGGCGGAGTTTCAACAGCTCTATACGGGGAAGGGGCCCTGGAAGAGCGCG 480
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CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A
 CC pharmaceutical composition comprising a DNzyme of the invention is
 CC useful for treating tumours in a subject, and for enhancing the
 CC sensitivity of malignant or virus infected cells to chemotherapy.
 CC The DNzymes are useful in diagnostics, therapeutics,
 CC prophylaxis, research agents and in kits. The DNzymes are also useful
 CC for increasing the susceptibility of tumour cells to anti-tumour
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide
 CC sequence represents a human bcl-2 gene of the invention

XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 98.6%; Score 575; DB 7; Length 3542;

Best Local Similarity 99.1%; Pred. No. 1.1e-133;
 Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGGAACCCGAGCTTGGGCCCCAGACACACGAGCTGTGGGAGACTTTGTAGTTAT 60
 DB 177 ATGGGGAACCCGAGCTTGGGCCCCAGACACACGAGCTGTGGGAGACTTTGTAGTTAT 236
 QY 61 AAGCTGAGGACAGAGGATATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGAGCTGAC 120
 DB 237 AAGCTGAGGACAGAGGATATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGAGCTGAC 296
 QY 121 CCGCTGACCAACGACATGCGGAGAGCTGAGATGATGATGACCCCGCTTCCGGCGAC 180
 DB 297 CCGCTGACCAACGACATGCGGAGAGCTGAGATGATGATGACCCCGCTTCCGGCGAC 356
 QY 181 TTCTCTGATCTGGCGGCTAGCTGATGTGACCCAGCTCAAGCCAGACAGCTTCAAC 240
 DB 357 TTCTCTGATCTGGCGGCTAGCTGATGTGACCCAGCTCAAGCCAGACAGCTTCAAC 416
 QY 241 CAGGCTCCGAGAACTTTTCAAGGGGCCCCCACTGAGGCGCTTGTAGCTTTCTT 300
 DB 417 CAGGCTCCGAGAACTTTTCAAGGGGCCCCCACTGAGGCGCTTGTAGCTTTCTT 476
 QY 301 CTCTTTGGGAGTCACTGTGTGTGAGAGTGTCAACAGAGATGAAACAACACTGGTGG 360
 DB 477 GTCTTTGGGAGTCACTGTGTGTGAGAGTGTCAACAGAGATGAAACAACACTGGTGG 536
 QY 361 CAAGTGCAGAGTGTGATGCTTACCTGAGAGAGCGGCTGTGTGATGATCCACAGC 420
 DB 537 CAAGTGCAGAGTGTGATGCTTACCTGAGAGAGCGGCTGTGTGATGATCCACAGC 596
 QY 421 AAGTGGGAGCTGGGCGGAGTTCAAGCTCTATACGGGAGAGCGGCTGTGAGAGAGCGG 480
 DB 597 AAGTGGGAGCTGGGCGGAGTTCAAGCTCTATACGGGAGAGCGGCTGTGAGAGAGCGG 656
 QY 481 CGTTCGAGGAGGAGGAGAACTGGGAGATGATGAGAGACAGTGTGAGCGGGGCGTGGCA 540
 DB 657 CGTTCGAGGAGGAGGAGAACTGGGAGATGATGAGAGACAGTGTGAGCGGGGCGTGGCA 716
 QY 541 GGGGCGCTGTGATGATGAGGAGGCTTTTGTGATGAGAGTGA 583
 DB 717 GGGGCGCTGTGATGATGAGGAGGCTTTTGTGATGAGAGTGA 759

RESULT 8
 AAX25132
 ID AAX25132 standard; DNA; 581 BP.

XX AAX25132;
 AC AAX25132;
 DT 05-JUL-1999 (first entry)
 XX Human bcl-w gene.
 DE Human bcl-w gene.
 XX Spermatozoogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 KW animal model; ss.
 XX Homo sapiens.
 OS
 XX
 PN W0913710-A1.

XX 25-MAR-1999.
 PD 16-SEP-1998; 98W-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson J, Koentgen F;
 PI WPI; 1999-243890/20.
 DR P-PSDB; AAY05530.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Claim 3; Page 32; 52pp; English.

XX The present sequence is the human bcl-w gene encoding Bcl-w protein (see
 CC AAY05530), a pro-survival member of the Bcl-2 family which is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene or in a gene associated with bcl
 CC -w. Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities as
 CC determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

XX Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other;

Query Match 98.3%; Score 573; DB 2; Length 581;

Best Local Similarity 99.1%; Pred. No. 2.3e-133;
 Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGGAACCCGAGCTTGGGCCCCAGACACACGAGCTGTGGGAGACTTTGTAGTTAT 60
 DB 1 ATGGGGAACCCGAGCTTGGGCCCCAGACACACGAGCTGTGGGAGACTTTGTAGTTAT 60
 QY 61 AAGCTGAGGACAGAGGATATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGAGCTGAC 120
 DB 61 AAGCTGAGGACAGAGGATATGTCTGTGAGCTGGCCCCGGGAGAGGCCAGAGCTGAC 120
 QY 121 CCGCTGACCAACGACATGCGGAGAGCTGAGATGATGATGACCCCGCTTCCGGCGAC 180
 DB 121 CCGCTGACCAACGACATGCGGAGAGCTGAGATGATGATGACCCCGCTTCCGGCGAC 180
 QY 181 TTCTCTGATCTGGCGGCTAGCTGATGTGACCCAGAGCTCAAGCCAGACAGCTTCAAC 240
 DB 181 TTCTCTGATCTGGCGGCTAGCTGATGTGACCCAGAGCTCAAGCCAGACAGCTTCAAC 240
 QY 241 CAGGCTCCGAGAACTTTTCAAGGGGCCCCCACTGAGGCGCTTGTAGCTTTCTT 300
 DB 241 CAGGCTCCGAGAACTTTTCAAGGGGCCCCCACTGAGGCGCTTGTAGCTTTCTT 300
 QY 301 CTCTTTGGGAGTCACTGTGTGTGAGAGTGTCAACAGAGATGAAACAACACTGGTGG 360
 DB 301 GTCTTTGGGAGTCACTGTGTGTGAGAGTGTCAACAGAGATGAAACAACACTGGTGG 360
 QY 361 CAAGTGCAGAGTGTGATGCTTACCTGAGAGAGCGGCTGTGTGATGATCCACAGC 420
 DB 361 CAAGTGCAGAGTGTGATGCTTACCTGAGAGAGCGGCTGTGTGATGATCCACAGC 420
 QY 421 AAGTGGGAGCTGGGCGGAGTTCAAGCTCTATACGGGAGAGCGGCTGTGAGAGAGCGG 480
 DB 421 AAGTGGGAGCTGGGCGGAGTTCAAGCTCTATACGGGAGAGCGGCTGTGAGAGAGCGG 480

PS Disclosure; Col 15-16; 26pp; English.

XX The present sequence encodes human bcl-2 protein (Hbcl-2). The
XX specification also describes rat bcl-2 protein (Rbcl-2). Rbcl-2 and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-2 and Hbcl-2
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-2 and
CC Hbcl-2 may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites

XX Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

Query Match 97.4%; Score 567.8; DB 2; Length 579;
Best Local Similarity 96.8%; Pred. No. 4.5e-122;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGACCTCGGCCGACACACACGCGCTCTGTGGACACTTTGTAGTTAT 60
DB 1 ATGGCGACCCGACCTCGGCCGACACACACGCGCTCTGTGGACACTTTGTAGTTAT 60
QY 61 AAGCTGAGGCGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 120
DB 61 AAGCTGAGGCGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGCCAGAGCTGAC 120
QY 121 CCGCTGACCAAGCCATCGGCGAGCTGAGATGATGATGACCCGCTTCGGCGGAC 180
DB 121 CCGCTGACCAAGCCATCGGCGAGCTGAGATGATGATGACCCGCTTCGGCGGAC 180
QY 121 CCACCTGACCAAGCCATCGGCGAGCTGAGATGATGATGACCCGCTTCGGCGGAC 180
DB 121 CCACCTGACCAAGCCATCGGCGAGCTGAGATGATGATGACCCGCTTCGGCGGAC 180
QY 181 TTCTCTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGAT 240
DB 181 TTCTCTGATCTGGCGGCTCAGCTGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CAGGCTCTCGATGAACTTTTCAAGGGGCGCCCACTGGGCGGCTTTGATGCTTTT 300
DB 241 CAGGCTCTCGATGAACTTTTCAAGGGGCGCCCACTGGGCGGCTTTGATGCTTTT 300
QY 301 CTCTTGGGGGCTGACCTGTGTGCTGAGATGTCACAGAGATGAAACCACTGATGGA 360
DB 301 CTCTTGGGGGCTGACCTGTGTGCTGAGATGTCACAGAGATGAAACCACTGATGGA 360
QY 361 CAGTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CAGTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 AAGTGGGGGCTGGCGGAGTTCAAGCTCTATACGCGGAGCGGGGCTTGAAGAGCGGG 480
DB 421 AAGTGGGGGCTGGCGGAGTTCAAGCTCTATACGCGGAGCGGGGCTTGAAGAGCGGG 480
QY 481 CGTCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 CGTCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GGGGCGCTGTACTGTAGAGGCGCTTTTGTAGCAAG 579
DB 541 GGGGCGCTGTACTGTAGAGGCGCTTTTGTAGCAAG 579

RESULT 11
ADBS2996
ID ADBS2996 standard; DNA; 582 BP.
XX
AC ADBS2996;

XX 04-DEC-2003 (first entry)

XX Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.

DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

KW toxicity marker; toxicity progression; drug screening;

KW primary rat hepatocyte toxicity modelling; gene; ds.

OS Rattus norvegicus.

PN MO2003065993-42.

PD 14-AUG-2003.

PF 04-FEB-2003; 2003WO-US003482.

PR 04-FEB-2003; 2002US-0353171P.

PR 13-MAR-2002; 2002US-036354P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 11-APR-2002; 2002US-0371413P.

PR 11-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0374139P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0376652P.

PR 09-MAY-2002; 2002US-0376653P.

PR 09-MAY-2002; 2002US-0376655P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-UN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elashoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for

PT identifying hepatotoxic compounds, comprises comparing a gene expression

PT profile of a tissue or cell sample to a database of Tox mean and non-Tox

PT mean values.

XX Claim 44; SEQ ID NO 3538; 874pp; English.

XX The present invention describes a method for determining whether a

XX compound induces a toxic effect on a tissue or cell. The method comprises

XX preparing a gene expression profile of a tissue or cell sample exposed to

XX the compound, and comparing the gene expression profile to a database

XX comprising data or information on the Tox mean and non-Tox mean value.

XX The method is useful for predicting or identifying at least one toxic

XX effect, particularly hepatotoxicity, of a test or unknown compound. The

XX genes listed in the specification are useful as diagnostic or toxicity

XX markers for the prediction or identification of the physiological state

XX of tissue or cell sample that has been exposed to a compound, or to

XX identify or predict the toxic effects of a compound or an agent. These

XX may also be used as markers for monitoring toxicity progression or for

XX drug screening. The present sequence represents a primary rat hepatocyte

XX toxicity modelling related gene sequence from the present invention.

XX Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;

Query Match 90.5%; Score 527.6; DB 9; Length 582;
Best Local Similarity 94.2%; Pred. No. 5e-122;
Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCGACCCGACCTCGGCCGACACACGCGCTCTGTGGACACTTTGTAGTTAT 60

```

Db      1  ATGGGACCCCAAGCCTCAACCCCAAGACACACGAGGCTCTAGTGTCTGACTTTGTAGGCTAT 60
QY      61  AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGGAGGGCCCAACAGCTGAC 120
Db      61  AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGGAGGGCCCAACAGCTGAC 120
QY      121  CCGGTGACCAAGGCAATGCGGCGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
Db      121  CCGGTGACCAAGGCAATGCGGCGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
QY      181  TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTAC 240
Db      181  TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTAC 240
QY      241  CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCCTTGTAGCCCTTT 300
Db      241  CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCCTTGTGTGGCATTT 300
QY      301  CTCTTTGGGGCTGCACTGTGTGCTGAGAGTCAACAGAGATGAAACCACTGTGGGA 360
Db      301  GTCTTTGGGGCTGCTCTGTGTGCTGAGAGTGTCAACAAAGATGAGCCATTGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGCGGCTGTGCACTGGATCCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGCGCTTGTGCACTGGATCCACAGC 420
QY      421  AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGAGCGGGGCTTGAAGAGCGCG 480
Db      421  AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGAGCGGGGCTTGAAGAGCGCG 480
QY      481  CGTCTGCGGAGGGGAACTGAGCATCAAGTGAAGACAGTGTGACGGGGGCTGTGGCA 540
Db      481  CGTCTGCGGAGGGGAACTGAGCATCAAGTGAAGACAGTGTGACGGGGGCTGTGGCA 540
QY      541  GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
Db      541  GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582

RESULT 12
AAV28333
ID      AAV28333 standard; cDNA; 579 BP.
XX
AC      AAV28333;
XX
DT      02-OCT-1998 (first entry)
XX
DE      Rat bcl-y gene.
XX
KW      ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS      Rattus sp.
XX
FH      Key
FT      CDS
FT      1..579
FT      Location/Qualifiers
FT      CDS
FT      1..579
FT      /tag= a
FT      /product= "bcl-y"
FT      /note= "No stop codon given"

US5789201-A.
XX
PN      04-AUG-1998.
XX
PF      11-FEB-1997; 97US-00798897.
XX
PR      23-FEB-1996; 96US-0012201P.
XX
PA      (COCE-) COCENSYS INC.
XX
PI      Guastella J;
XX
PI      WPI; 1998-446079/38.
XX
DR      P-PSDB; AAM61391.

```

```

XX      XX
PT      Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT      recombinant protein for use in treating uncontrolled cell growth e.g.
PT      cancers.
PS      Claim 2; Column 13/14; 27pp; English.
XX      CC
XX      The mammalian bcl-y genes encode a protein that is a member of the bcl-2
XX      family, components in the cell death pathway. The bcl-2 family have both
XX      apoptotic activity and the apoptosis blocking activity. bcl-y falls in
XX      the apoptosis activity category. The recombinant protein may be used to
XX      prevent uncontrolled cell growth, either by its direct administration to
XX      recombinant genetic constructs to increase its expression in vivo. Also,
XX      antisense constructs can be used in disorders where prevention of cell
XX      death is desired
SQ      Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
QY      Query Match      89.7%; Score 523; DB 2; Length 579;
QY      Best Local Similarity 94.0%; Pred. No. 7e-121;
QY      Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Db      1  ATGGGACCCCAAGCCTCAACCCCAAGACACACGAGGCTCTAGTGTCTGACTTTGTAGGCTAT 60
QY      61  AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGGAGGGCCCAACAGCTGAC 120
Db      61  AAGCTGAGGCGAAGAGGTTATCTGTGAGACTGCCCCGGGGAGGGCCCAACAGCTGAC 120
QY      121  CCGGTGACCAAGGCAATGCGGCGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
Db      121  CCGGTGACCAAGGCAATGCGGCGAGCTGAGATGATTCGAGACCCGCTTCCGGCGAC 180
QY      181  TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTAC 240
Db      181  TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGGCTCAGGCCAGCAACGTTAC 240
QY      241  CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCCTTGTAGCCCTTT 300
Db      241  CAGGCTCTCCGACGAATCTTTTCAAGGGGGCCCACTGGGGCGCCTTGTGTGGCATTT 300
QY      301  CTCTTTGGGGCTGCACTGTGTGCTGAGAGTCAACAGAGATGAAACCACTGTGGGA 360
Db      301  GTCTTTGGGGCTGCTCTGTGTGCTGAGAGTGTCAACAAAGATGAGCCATTGTGGGA 360
QY      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGCGGCTGTGCACTGGATCCACAGC 420
Db      361  CAAGTGCAGAGTGGATGTGCTTACCTGAGACGCGCTTGTGCACTGGATCCACAGC 420
QY      421  AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGAGCGGGGCTTGAAGAGCGCG 480
Db      421  AGTGGGGGCTGGGCGGAGTTTACAGCTCTATACGGGAGCGGGGCTTGAAGAGCGCG 480
QY      481  CGTCTGCGGAGGGGAACTGAGCATCAAGTGAAGACAGTGTGACGGGGGCTGTGGCA 540
Db      481  CGTCTGCGGAGGGGAACTGAGCATCAAGTGAAGACAGTGTGACGGGGGCTGTGGCA 540
QY      541  GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 579
Db      541  GGGGCGCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 579

RESULT 13
AAV15945
ID      AAV15945 standard; cDNA; 579 BP.
XX
AC      AAV15945;
XX
DT      20-MAY-1999 (first entry)
XX
DE      CDNA encoding the rat bcl-y protein.

```


KW Rat bcl-y protein, Rbcl-y; human bcl-y protein, Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
 KW ss.
 XX Rattus sp.
 OS US5883229-A.
 XX 16-MAR-1999.
 XX 25-NOV-1997; 97US-00978523.
 XX 23-FEB-1996; 96US-0012201P.
 XX 11-FEB-1997; 97US-00798897.
 XX (COCE-) COGENSYS INC.
 XX Guastella J;
 XX WPI; 1999-214150/18.
 XX P-PSDB; AAW97391.
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 XX modulating programmed cell death.
 XX Disclosure; Col 13-16; 26pp; English.
 XX The present sequence encodes rat bcl-y protein (Rbcl-y). The
 XX specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
 XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in
 XX programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
 XX proteins may be used to treat conditions associated with a disruption of
 XX the cell death pathway. If they act as cell death inhibitors, they may be
 XX used in therapies to treat subjects suffering from strokes, head trauma,
 XX Alzheimer's Disease, neural and muscular degenerative diseases
 XX (especially multiple sclerosis), myocardial infarction, vitally induced
 XX cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
 XX - conditions where cells under go premature cell death as a result of
 XX triggers which may or may not be apparent. They may also be used in this
 XX way to develop cell lines which remain viable in culture for an extended
 XX period. In contrast, if they act as cell death stimulators, Rbcl-y and
 XX Hbcl-y may be used to treat conditions associated with prolonged cell
 XX life span such as cancer (especially Kaposi's sarcoma and lung cancer)
 XX and auto/hyperimmune diseases. They may also be used to cause cell death
 XX in, and hence control, parasites
 XX Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
 SQ
 Query Match 89.7%; Score 523; DB 2; Length 579;
 Best Local Similarity 94.0%; Pred. No. 7e-121;
 Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 241 CAGGTCTCCGAGCAATTTTTCAGAGGGGCCCCCACTGGGGCGCTTTAGCCTTT 300
 DB 241 CAGGTCTCCGAGCAATTTTTCAGAGGGGCCCCCACTGGGGCGCTTTAGCCTTT 300
 QY 301 CTTCTGGGCGCTGCACTGTCGTGAGAGTGCACCAAGAGATGGAACCACTGGTGGGA 360
 DB 301 GTTTTGGGCGCTGCTGTGTGTGAGAGTGCACCAAGATGGAACCACTGGTGGGA 360
 QY 361 CAAATGCAAGATGATGTGTCCTTACCTGAGACGCGCTGCTGACTGATCCACAC 420
 DB 361 CAAATGCAAGATGATGTGTCCTTACCTGAGACACGCTGCTGACTGATCCACAC 420
 QY 421 AGTGGGGGCTGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCTTGGAGAGCGCG 480
 DB 421 AGTGGGGGCTGGGCGAGATTCAAGCTCTATACGGGGACGGGGCCTTGGAGAGCGCG 480
 QY 481 CGTCTCGGGAGGGGAACTGGGGATCAGTGAAGACATGTCAGGGGGCGTGGCACTG 540
 DB 481 CGTCTCGGGAGGGGAACTGGGGATCAGTGAAGACATGTCAGGGGGCGTGGCACTG 540
 QY 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579
 DB 541 GGGGCCCTGTAACTGTAGGGGCTTTTGTGTAGCAAG 579
 RESULT 14
 AAX25133
 ID AAX25133 standard; DNA; 581 BP.
 XX AAX25133;
 XX 05-JUL-1999 (first entry)
 XX Mouse bcl-w gene.
 XX Spermatoogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
 KW animal model; ss.
 XX Mus sp.
 OS WO99133710-A1.
 XX 25-MAR-1999.
 XX 16-SEP-1998; 98WO-AU000764.
 XX 16-SEP-1997; 97AU-00009228.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Cory S, Adams J, Print C, Gibson L, Koentgen F;
 PI WPI; 1999-243890/20.
 DR P-PSDB; AAY05531.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS Claim 3; Page 34; 52pp; English.
 XX The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
 CC AAY05531), a pro-survival member of the Bcl-2 family which is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene or in a gene associated with bcl
 CC -w. Such animals have disorganised seminiferous tubules and are
 CC substantially infertile, but possess no other major abnormalities as
 CC determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,

CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 89.5%; Score 521.8; DB 2; Length 581;
 Best Local Similarity 93.6%; Pred. No. 1.4e-120;
 Matches 544; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATGATTAT 60
 Db 1 ATGGCGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATGATTAT 60
 QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCCAAGCACTGAC 120
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 QY 121 CCGCTGCACCAAGCCATGCGGGGAGCTGAGATGATTCGAGACCCGCTTCGGGGCGAC 180
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 QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAAGCCAGCAAGCTTCACC 240
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 QY 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTTGAGCCTTTT 300
 Db 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTTGAGCCTTTT 300
 QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGATGACCACTGTGGGA 360
 Db 301 GTCTTTGGGGCTGCTGTGTGTGAGAGTGTCAACAAGATGACCACTTTGTGGGA 360
 QY 361 CAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AGTGGGGCTGCGGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGGCGG 480
 Db 421 AGTGGGGCTGCGGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGGCGG 480
 QY 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGCACTG 540
 Db 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGCACTG 540
 QY 541 GGGGCGCTGTAAGTCTGAGGGGCTTTTGTGCTGCAAGTG 581
 Db 541 GGGGCGCTGTAAGTCTGAGGGGCTTTTGTGCTGCAAGTG 581

RESULT 15

AAT96578
 ID AAT96578 standard; DNA; 581 BP.

AC AAT96578;

DT 22-APR-1998 (first entry)

XX Mouse bcl-w DNA.

XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;

KW diagnosis; degenerative disease; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT 1..507
 FT /*cag= a
 FT /product= "bcl-w"
 FT /note= "q"

XX MO9735971-A1.

PD 02-OCT-1997.

XX 27-MAR-1997; 97WO-AU000199.

XX 27-MAR-1996; 96AU-00008965.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Cory S, Adams JM, Gibson LM, Holmgren SF;

XX MPI; 1997-489635/45.

XX P-PSDB; AAM36048.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.

PS Claim 3; Page 50-51; 86pp; English.

XX This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
 XX family. This gene promotes cell survival, so its modulation is useful in
 XX treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
 XX stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
 XX hypoxia, ischaemia, human immunodeficiency virus infection or in cell
 XX transplants. Up-regulation of the gene can also be used to modify cell
 XX lines cultured in vivo, e.g. to develop new lines, to facilitate
 XX isolation of hybridomas and to increase survival of primary explants
 XX CC during genetic modification. It can be used to produce recombinant Bcl-w
 XX for therapy, diagnosis, antibody production or screening of potential
 XX modulators

XX Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0 Other;

Query Match 85.9%; Score 501; DB 2; Length 581;
 Best Local Similarity 91.4%; Pred. No. 2.2e-115;
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATGATTAT 60

Db 1 ATGGGACCCCGAGCTCGGCCGAGACACAGGGCTCTGTGGGAGACCTTTGATGATTAT 60

QY 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCCAAGCACTGAC 120

Db 61 AAGCTGAGGCGAAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCCAAGCACTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGAGCGAGTTTGAAGACCCGTTCCGGCGAC 180

Db 121 CCGCTGCACCAAGCCATGCGGGCTGTGAGAGCGAGTTTGAAGACCCGTTCCGGCGAC 180

QY 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAAGCCAGCAAGCTTCACC 240

Db 181 TTCTCTGATCTGCGGCTCAGCTCATGTGACCCAGCTCAAGCCAGCAAGCTTCACC 240

QY 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTTGAGCCTTTT 300

Db 241 CAGGTTCTCCGACGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTTGAGCCTTTT 300

QY 301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGATGACCACTGTGGGA 360

Db 301 GTCTTTGGGGCTGCTGTGTGTGAGAGTGTCAACAAGATGACCACTTTGTGGGA 360

QY 361 CAAAGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Db 361 CAAAGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 421 AAGTGGGGCTGCGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGGCGG 480

Db 421 AAGTGGGGCTGCGGAGTTCAAGCTCTATACGGGGAGCGGGCCCTGAGAGAGGGCGG 480

QY 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGCACTG 540

Db 481 CGTCTGCGGAGAGGGAATCTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGGTGCACTG 540

Qy 541 GGGGCCCTGTACTGTAGGGCCCTTTTGCTAGCAAGTg 581
Db 541 GGGGCCCTGTACTGTAGGGCCCTTTTGCTAGCAAGTg 581

Search completed: March 29, 2004, 04:39:43
Job time : 369.622 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: March 25, 2004, 15:35:20 ; Search time 36 Seconds
(without alignments)
1691.528 Million cell updates/sec

Title: US-09-155-327g-7
Perfect score: 1007
Sequence: 1 MARPASAPDRALVADPVG.....LTGVALGALVTGAFPAK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phase:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 996 | 98.9 | 193 | 11 | 088996 |
| 2 | 996 | 98.9 | 219 | 11 | 077860 |
| 3 | 996 | 94.9 | 193 | 11 | 08CG14 |
| 4 | 761 | 75.6 | 178 | 11 | 09CYW5 |
| 5 | 761 | 75.6 | 178 | 11 | 08CFR2 |
| 6 | 440.5 | 43.7 | 233 | 6 | 09MYW4 |
| 7 | 435.5 | 43.2 | 233 | 11 | 035844 |
| 8 | 433.5 | 43.0 | 233 | 6 | 08SQ42 |
| 9 | 431.5 | 42.9 | 233 | 6 | 09N1A2 |
| 10 | 428.5 | 42.6 | 233 | 6 | 09MZS7 |
| 11 | 413 | 41.0 | 236 | 11 | 08BOK4 |
| 12 | 413 | 41.0 | 236 | 11 | 07TSN8 |
| 13 | 403 | 40.0 | 238 | 13 | 090298 |
| 14 | 402 | 39.9 | 79 | 11 | 07TS61 |
| 15 | 401 | 39.8 | 180 | 6 | 09BD5 |
| 16 | 401 | 39.8 | 217 | 11 | 099N35 |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 399 | 39.6 | 236 | 11 | 0923R6 | Q923R6 cricetus |
| 18 | 398.5 | 39.6 | 180 | 6 | Q9BDX7 | Q9BDX7 bos taurus |
| 19 | 396.5 | 39.4 | 235 | 6 | Q81008 | Q81008 felis silve |
| 20 | 380.5 | 37.8 | 284 | 11 | Q7TS62 | Q7TS62 ratius norv |
| 21 | 374.5 | 37.2 | 188 | 11 | Q9QW2 | Q9QW2 mus musculu |
| 22 | 374.5 | 37.2 | 235 | 11 | Q35843 | Q35843 mus musculu |
| 23 | 373.5 | 37.1 | 188 | 4 | Q9H1R6 | Q9H1R6 homo sapien |
| 24 | 373 | 37.0 | 204 | 13 | 0902H2 | 0902H2 xenopus lae |
| 25 | 366.5 | 36.4 | 153 | 6 | Q7YR86 | Q7YR86 canis fami |
| 26 | 354 | 35.2 | 185 | 6 | Q8WJ81 | Q8WJ81 bos taurus |
| 27 | 347 | 34.5 | 219 | 11 | Q99N36 | Q99N36 mus musculu |
| 28 | 343.5 | 34.1 | 199 | 11 | Q8C5P0 | Q8C5P0 mus musculu |
| 29 | 296 | 29.4 | 89 | 13 | Q8WJ1 | Q8WJ1 gallus gall |
| 30 | 189 | 18.8 | 209 | 11 | Q9WJ5 | Q9WJ5 ratius norv |
| 31 | 185 | 18.4 | 170 | 11 | Q9WJ5 | Q9WJ5 ratius norv |
| 32 | 184 | 18.3 | 209 | 11 | Q8C264 | Q8C264 mus musculu |
| 33 | 176.5 | 17.5 | 192 | 13 | Q919N4 | Q919N4 brachydantio |
| 34 | 175.5 | 17.4 | 190 | 4 | Q8NFF3 | Q8NFF3 homo sapien |
| 35 | 171.5 | 17.0 | 221 | 13 | Q98UJ3 | Q98UJ3 xenopus lae |
| 36 | 168.5 | 16.7 | 125 | 4 | Q9H1R6 | Q9H1R6 homo sapien |
| 37 | 163 | 16.2 | 58 | 11 | Q9H1B3 | Q9H1B3 ratius norv |
| 38 | 162 | 16.1 | 235 | 5 | Q967D2 | Q967D2 geodia cydo |
| 39 | 159.5 | 15.8 | 163 | 6 | Q9MZS6 | Q9MZS6 ovis aries |
| 40 | 155.5 | 15.4 | 173 | 11 | Q8K3J2 | Q8K3J2 mus musculu |
| 41 | 153 | 15.2 | 173 | 4 | Q8WZ49 | Q8WZ49 homo sapien |
| 42 | 153 | 15.2 | 173 | 11 | Q9JX13 | Q9JX13 ratius norv |
| 43 | 152 | 15.1 | 67 | 6 | Q8WJ83 | Q8WJ83 cervus elap |
| 44 | 148.5 | 14.7 | 218 | 5 | Q9N754 | Q9N754 suberites d |
| 45 | 148 | 14.7 | 192 | 6 | Q8SQ43 | Q8SQ43 felis silve |

ALIGNMENTS

RESULT 1
088996 PRELIMINARY; FRT; 193 AA.
ID 088996
AC 088996;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE BCL-W.
GN BCL-W.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=2672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RA "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation";
RT J. Neurochem. 85:1500-1512(2003).
RL EMBL: AF096291; AAC64200.1; -;
DR EMBL: AF185096; AAC64468.1; -;
DR HSSP: Q07817; IMAZ.
DR GO: GO:0006915; P:apoptosis regulator activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR00712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_Family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS00063; BH4_2; 1.
 SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match
 Best Local Similarity 98.9%; Score 996; DB 11; Length 193;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 60
 DB 1 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 60
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 120
 DB 61 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 120
 QY 121 QVQEMWVAVLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 180
 DB 121 QVQDMWVYLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193

RESULT 2

QY 07TS60 PRELIMINARY; PRT; 219 AA.
 AC 07TS60;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE BCL-WEL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=2672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 RT differentiation";
 RL J. Neurochem. 85:1500-1512(2003).
 DR EMBL; AY185100; AA064470.1; -;
 SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;

Query Match
 Best Local Similarity 98.9%; Score 996; DB 11; Length 219;
 Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 60
 DB 27 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 86
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 120
 DB 87 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 146
 QY 121 QVQEMWVAVLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 180
 DB 147 QVQDMWVYLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 206
 QY 181 GALVTGAFPAK 193
 DB 207 GALVTGAFPAK 219

RESULT 3

ID 08CGL4 PRELIMINARY; PRT; 193 AA.
 AC 08CGL4;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Bcl2-like protein 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Skin;
 RA Su H.-Y.;
 RT "Extraction from neonatal mouse skin after IGF-1 stimulation";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY170344; AA013177.1; -;
 DR MGD; MG1:108052; BCL212.
 DR GO; GO:0016329; P:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; BCL2_BH.
 DR InterPro; IPR003093; BCL2_BH.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 SQ SEQUENCE 193 AA; 20950 MW; 258AC1816D6FA0 CRC64;

Query Match
 Best Local Similarity 94.9%; Score 956; DB 11; Length 193;
 Matches 184; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 60
 DB 1 MATPASPTDTRALVADFGYKLRQKGYVCGAGPGGPPADPLHQAMRAAGDEFFTRFRRT 60
 QY 61 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 120
 DB 61 FSDLAQQLHTVTPGSAQQRFTQVSDLEFQGGPNMGRVAFVFGALCAESVKNKEEPLVG 120
 QY 121 QVQEMWVAVLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 180
 DB 121 QVQDMWVYLETRLADWIMHSSGGMAEFTALYDGDALBEARRLRGNMNASVRTVLTGAVAL 180
 QY 181 GALVTGAFPAK 193
 DB 181 GALVTGAFPAK 193

RESULT 4

QY 09CYW5 PRELIMINARY; PRT; 178 AA.
 AC 09CYW5;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 24, Last annotation update)
 DE Bcl2-like 2.
 GN BCL2L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

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RX MEDLINE=2108560; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kono S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momaberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL: AK013244; BAB28740.1; -.
DR HSSP: Q07817; 1MA2.
DR MGD: MGI:108052; Bcl212.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 9.6e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQMPRAAGDEFETFRRT 60
DB 1 MATPASPTDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQMPRAAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEPELVG 120
DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEPELVG 120
QY 121 QVQEMWVAVLETRLADWHSKGGMAEFTAL 150
DB 121 QVQEMWVAVLETRLADWHSKGGMAEFTAL 150

RESULT 5
Q8CER2 PRELIMINARY; PRT; 178 AA.
AC Q8CER2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcl2-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC Tissue=Eye;
RA Strausberg R.;

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RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC040369; AAH40369.1; -.
DR MGD: MGI:108052; Bcl212.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;
Best Local Similarity 95.3%; Pred. No. 9.6e-60;
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQMPRAAGDEFETFRRT 60
DB 1 MATPASPTDTRALVADFGVYKLRQKGYVCGAGPGEPAADPLHQMPRAAGDEFETFRRT 60
QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEPELVG 120
DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVKNKEPELVG 120
QY 121 QVQEMWVAVLETRLADWHSKGGMAEFTAL 150
DB 121 QVQEMWVAVLETRLADWHSKGGMAEFTAL 150

RESULT 6
Q9MTW4 PRELIMINARY; PRT; 233 AA.
AC Q9MTW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC Knott J.C., Robertson L., James E.R.;
RA "Rabbit Bcl-X.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005131; AAF88137.1; -.
DR HSSP: P53563; IAF3.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS0063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match          43.7%: Score 440.5; DB 6; Length 233;
Best Local Similarity 42.0%: Pred. No. 3.8e-31;
Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKRYC-----GAG-----FGEGRPA 39
DB 6 RELVADPFLSYKLSQKGYSWSPSDVENRTEAPDEGTGEMETPSAINGNPAMHADSFAV 65
QY 40 D-----PLHQAMRAAGDEFEFRFRFTSDLAQAOLHTVFGSAQQRFTQ 81
DB 66 NCATGSSSLDAREVTPMTAVKQALREAGDEFELRYRAAFSDLTISQHLITPTGTAYQSPFEQ 125
QY 82 VSDDELFGQGPMMGRIVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSS 141
DB 126 VVNELEFRQGVNMGRIIVAFSPFGALCVESVDKEMEVLSRIAAMWATYLNHLEPWIOEN 185
QY 142 GGMAEFTALYGDGALAEARLRRE--GNWASVRYTLTGAVALGAL 183
DB 186 GGMDFVVELYGNNAAESRKQGERNRFMTGTAVAGVLLGSL 229

RESULT 7
035844 PRELIMINARY; PRT; 233 AA.
AC 035844;
DT 01-JUN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bcl-XL.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
apoptosis in T cells."
RT Immunol 7:629-639(1997).
RL EMBL; U51278; AAC53459.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MG1:86139; Bcl2L.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0016329; F-apoptosis regulator activity; IEA.
DR GO; GO:0006915; P-apoptosis; IEA.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match          43.2%: Score 435.5; DB 11; Length 233;
Best Local Similarity 41.8%: Pred. No. 1.1e-30;
Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQKRYC-----V 28
DB 6 RELVADPFLSYKLSQKGYSWSPSDVENRTEAPDEGTGEMETPSAINGNPAMHADSFAV 65

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QY 29 CGAGPEGEPAD-----PLHQAMRAAGDEFEFRFRFTSDLAQAOLHTVFGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVTPMTAVKQALREAGDEFELRYRAAFSDLTISQHLITPTGTAYQSPFE 124
QY 81 QVSDDELFGQGPMMGRIVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSS 140
DB 125 QVNELEFRQGVNMGRIIVAFSPFGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIOE 184
QY 141 SGMAEFTALYGDGALAEARLRRE--NWSVRYTLTGAVALGAL 183
DB 185 NGMDTFVVELYGNNAAESRKQGERNRFMTGTAVAGVLLGSL 229

RESULT 8
08SQ42 PRELIMINARY; PRT; 233 AA.
AC 08SQ42;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Bcl-XL protein.
GN BCL-XL.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
RT "Molecular cloning of feline Bcl-2 family "
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080951; BAB85856.2; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0016329; F-apoptosis regulator activity; IEA.
DR GO; GO:0006915; P-apoptosis; IEA.
DR InterPro; IPR00712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_FAMILY.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26017 MW; CD17F24F89D47BC9 CRC64;

Query Match          43.0%: Score 433.5; DB 6; Length 233;
Best Local Similarity 41.6%: Pred. No. 1.6e-30;
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

QY 11 RALVADPVGKLRQKRYC-----V 28
DB 6 RELVADPFLSYKLSQKGYSWSPSDVENRTEAPDEGTGEMETPSAINGNPAMHADSFAV 65
QY 29 CGAGPEGEPAD-----PLHQAMRAAGDEFEFRFRFTSDLAQAOLHTVFGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVTPMTAVKQALREAGDEFELRYRAAFSDLTISQHLITPTGTAYQSPFE 124
QY 81 QVSDDELFGQGPMMGRIVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSS 140
DB 125 QVNELEFRQGVNMGRIIVAFSPFGALCVESVDKEMQVLSRIAAMWATYLNHLEPWIOE 184
QY 141 SGMAEFTALYGDGALAEARLRRE--NWSVRYTLTGAVALGAL 193
DB 185 NGMDTFVVELYGNNAAESRK--GQERNRNRFMTGTAVAG--VLLGSLFSRK 233

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RESULT 9
OC Q9N1A2 PRELIMINARY; PRT; 233 AA.
AC Q9N1A2.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Anti-apoptotic regulator Bcl-xl.
GN BCL-XL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lee T.L., Gandy J.M.;
RT "PCR Cloning of a Porcine bcl-xl cDNA from Heart.";
RL Submitted (DBS-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF216205; AAF33212.1; -.
DR HSP; Q07817; IMAZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS01063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.9%; Score 431.5; DB 6; Length 233;
Best Local Similarity 41.8%; Pred. No. 2,4e-30;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----Y 28
DB 6 RELVVDPLSYKLSQKGYWSQFTDVEENRTAEPEGTSEAEPTPSALINGNPSWHLADSPAV 65
QY 29 CGAGPGEGPAPAD-----PLHQAMRAAGDEFETFRPTSPDLAQLHVTGPSAQCRPT 80
DB 66 NGA-TGHSSSLDARREVIAPMAAVKQALREAGDEFELRYRAFSDLTSQLHTTGTATQSTPE 124
QY 81 QVSDDELFGGPPNNGRLVAFVFGAALCAESVKNKEMPLVGVQEMWVAVLETRLADWHS 140
DB 125 QVAVNELFRDGVNMGRIYAFVFGALCVESVDKEMQVLVSRIATWATLTNLHLEPWICE 184
QY 141 SGMAEFTALYGDALIEARLRLE--GNWASVRYTLTGAVAGAL 183
DB 185 NGGMDTFVELYGNMAAESRKQGERFRNFWLTGMTLAGVLLGSL 229

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RESULT 10
OC Q9MZS7 PRELIMINARY; PRT; 233 AA.
AC Q9MZS7.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Bcl-x long protein.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT "Bcl-x in the sheep ovary.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164517; AAF89532.1; -.
DR HSP; P53563; IAF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS01063; BH4_2; 1.
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;

Query Match 42.6%; Score 428.5; DB 6; Length 233;
Best Local Similarity 40.6%; Pred. No. 4.5e-30;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADPVGKLRQKGY-----VCGAGP---GEGPAA 39
DB 6 RELVVDPLSYKLSQKGYWSQFSDVEENRTAEPEGTSDMETPSALINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETFRPTSPDLAQLHVTGPSAQCRPT 81
DB 66 NGATGHSRLDAREVIAPMAAVKQALREAGDEFELRYRAFSDLTSQLHTTGTAYQSFQEQ 125
QY 82 VSDDELFGGPPNNGRLVAFVFGAALCAESVKNKEMPLVGVQEMWVAVLETRLADWHS 141
DB 126 VVNELFRDGVNMGRIYAFVFGALCVESVDKEMQVLVSRIATWATLTNLHLEPWIOEN 185
QY 142 SGMAEFTALYGDALIEARLRLE--GNWASVRYTLTGAVAGAL 183
DB 186 GGMDTFVELYGNMAAESRKQGERFRNFWLTGMTVAGVLLGSL 229

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RESULT 11
OC Q9BQK4 PRELIMINARY; PRT; 236 AA.
AC Q9BQK4.
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE B-cell leukemia/lymphoma 2.
GN BCL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";

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RL Nature 420:563-573 (2002).
DR EMBL: AK049473; BAC33767.1; -.
DR MGD: MGI:88138; Bcl2.
DR GO: GO:0005829; Cytoosol; IDA.
DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0006915; P:apoptosis; IDA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 236 AA; 26437 MW; B726BFP3A3A1C718 CRC64;

Query Match 41.0%; Score 413; DB 11; Length 236;
Best Local Similarity 37.5%; Pred. No. 1,1e-28;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADVFVGYKLRKGVCGAG-----PG----- 34
DB 10 DNRREIVMKYIHYLSQRYGEMDADADAPLGAAPFGIFSPESNPFAVRDMART 69
QY 35 -----EGPADP-----LHQAMPAAGDEFETRRFRPSLAQLVHTPSAQQRFTQ 81
DB 70 SPLRLPVATGTPALSPVPVPHVLTLRAGDDFSRRRRDPAEMSSQLHPTFARGPAT 129
QY 82 VSDELFGQGNMGRALVAFVFGAALCAESVKNEMEPLVGVQVEMVAVYETRLADWISS 141
DB 130 VVELFRDGVNMGRIVAFEFEGVGVCSVKNEMSEPLVDNIALMTEYLNRHLHTWIDN 189
QY 142 GGNAEFTALYGDGALBEARLRGNMNASVTVLTGVALGALTVCAGPASK 193
DB 190 GGMDAFVELYG----PSMRPLPDFSWLSLTKTLISLAL-VGACITLIGAVLGKH 236

RESULT 12
Q77SN8 PRELIMINARY; PRT; 236 AA.
ID OTTSN8;
AC OTTSN8;
DT 01-OCT-2003 (TREMblrel. 25, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DE Bcl2-like protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
ON NCBI_TaxID=10116;
RX NCB1_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar;
RT "Rat Bcl2-like protein."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF512835; AAP47159.1; -.
SQ SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;

Query Match 41.0%; Score 413; DB 11; Length 236;
Best Local Similarity 37.5%; Pred. No. 1,1e-28;
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADVFVGYKLRKGVCGAG-----PG----- 34
DB 10 DNRREIVMKYIHYLSQRYGEMDADADAPLGAAPFGIFSPESNPFAVRDMART 69

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QY 35 -----EGPADP-----LHQAMPAAGDEFETRRFRPSLAQLVHTPSAQQRFTQ 81
DB 70 SPLRLPVATGTPALSPVPVPHVLTLRAGDDFSRRRRDPAEMSSQLHPTFARGPAT 129
QY 82 VSDELFGQGNMGRALVAFVFGAALCAESVKNEMEPLVGVQVEMVAVYETRLADWISS 141
DB 130 VVELFRDGVNMGRIVAFEFEGVGVCSVKNEMSEPLVDNIALMTEYLNRHLHTWIDN 189
QY 142 GGNAEFTALYGDGALBEARLRGNMNASVTVLTGVALGALTVCAGPASK 193
DB 190 GGMDAFVELYG----PSMRPLPDFSWLSLTKTLISLAL-VGACITLIGAVLGKH 236

RESULT 13
Q90Z98 PRELIMINARY; PRT; 238 AA.
ID Q90Z98;
AC Q90Z98;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Bcl-XL-like protein 1 (Bcl21 protein).
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
ON NCBI_TaxID=7955;
RX NCB1_TaxID=7955;
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=21239061; PubMed=11406282;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.R.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF317837; AA81706.1; -.
DR EMBL: BC044330; AA44130.1; -.
DR ZFIN: ZDB-GENE-010730-1; Bcl2l.
DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
DR GO: GO:0006915; F:apoptosis; IEA.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2; 1.

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DR Pfam; PF02180; BHL; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BHL; 1.
 DR PROSITE; PS50063; BHL_2; 1.
 SQ SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDB CRC64;

Query Match 40.0%; Score 403; DB 13; Length 238;
 Best Local Similarity 36.6%; Pred. No. 8.4e-28;
 Matches 87; Conservative 27; Mismatches 62; Indels 62; Gaps 6;

QY 11 RALVADPVGYKLRQKGYVC-----GAG----- 32
 DB 6 RELVVFPIKYLISGRANPCNHIGLTEDNRTDGAENGBGAAGTIVNGMRTNAST 65
 QY 33 --FEGRPADLPHG-----AMRAAGDEFETRFRRTSDLAQLHTVPGSAQR 78
 DB 66 GTPFQSPASSPQRTNGSGGLDAVKALRDSANFEELRYRAFNDSQSQHTPATAYQS 125
 QY 79 FTQVSDLLFQGGPWWGRVAFVFGALCAESVKNKMEPLVGVQVQEMWVAYLETRLADVI 138
 DB 126 FESVMDVFRDGVWGRIVGLFAGALCYECVEKEKMSPLVGRIAEMVTYLDNHIOPI 185
 QY 139 HSSGGMAEFTALYGDGALBEBARLRREG--NMA-SVRTVLGVALGALTVGAFFASK 193
 DB 186 QSQGMRERFAEIFSKDAASRSKQSFKKMLFAGMTLLTG-----VVGGILIQK 236

RESULT 14

ID Q7S61 PRELIMINARY; PRT; 79 AA.
 AC Q7S61;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BCL-WS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 RT differentiation";
 RL J. Neurochem. 85:1500-1512 (2003).
 DR EMBL; AY185099; AAC64469.1; -
 SQ SEQUENCE 79 AA; 8602 MW; 47EDFB3EE2909485 CRC64;

Query Match 39.8%; Score 402; DB 11; Length 79;
 Best Local Similarity 97.5%; Pred. No. 2.6e-28;
 Matches 77; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 115 MEPLVGVQVQEMWVAYLETRLADVIHSSGGAFFETALYGDALBEBARLRBGNMASVRYLV 174
 DB 1 MEPLVGVQVQEMWVAYLETRLADVIHSSGGAFFETALYGDALBEBARLRBGNMASVRYLV 60
 QY 175 TGAVALGALTVGAFFASK 193
 DB 61 TGAVALGALTVGAFFASK 79

RESULT 15

Q9BDD5 PRELIMINARY; PRT; 180 AA.
 AC Q9BDD5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-xL (Fragment).
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amills M., Bouzat J.;
 RT "Characterization of the bovine bcl-xL gene and related pseudogenes";
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF245488; AAK31307.1; -
 DR EMBL; AF245489; AAK31308.1; -
 DR HSSP; 007817; IMA2.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR00712; BCL2_BH.
 DR InterPro; IPR02475; BCL2_FAMILY.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BHL; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;

Query Match 39.8%; Score 401; DB 6; Length 180;
 Best Local Similarity 53.5%; Pred. No. 9e-28;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QMRAGDEFETRFRRTSDLAQLHTVPGSAQRFTQVSDLLFQGGPWWGRVAFVYG 103
 DB 38 QALRAGDEFELRYRARFARSDLTSLHTPGTAYQSFQGVNELFRDGVWGRIVAFSFG 97
 QY 104 AALCAESVKNKMEPLVGVQVQEMWVAYLETRLADVIHSSGGAFFETALYGDALBEBARLR 163
 DB 98 GALCAESVYDKEMQVLSRIATWATYLDHLEPWIQENGWDIVVELYGNNAAESRSKQ 157
 QY 164 E--GNMASVRTVLGVALGAL 183
 DB 158 EEFNRWFLTGMTVAGVLLGSL 179

Search completed: March 25, 2004, 15:44:26
 Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2004, 15:19:05 ; Search time 10 Seconds
(without alignments)
1004.954 Million cell updates/sec

Title: US-09-155-327G-7

Sequence: 1 MATPASPDPTRALVADPVG.....LTGVALGALVTGAFPSAK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| 1 | 1007 | 100.0 | 193 | 1 | BC1M_HUMAN |
| 2 | 1000 | 99.3 | 193 | 1 | BC1M_MOUSE |
| 3 | 646.5 | 64.2 | 228 | 1 | ARI_XENLA |
| 4 | 432.5 | 42.9 | 229 | 1 | BC1X_CHICK |
| 5 | 431.5 | 42.9 | 233 | 1 | BC1X_PIG |
| 6 | 428.5 | 42.6 | 233 | 1 | BC1X_HUMAN |
| 7 | 428.5 | 42.6 | 233 | 1 | BC1X_MOUSE |
| 8 | 428.5 | 42.6 | 233 | 1 | BC1X_RAT |
| 9 | 423.5 | 42.1 | 233 | 1 | BC1X_CHICK |
| 10 | 416.5 | 41.4 | 229 | 1 | BC1L_BOVIN |
| 11 | 414 | 41.1 | 236 | 1 | BC1L_RAT |
| 12 | 413 | 41.0 | 236 | 1 | BC1L_MOUSE |
| 13 | 412.5 | 41.0 | 239 | 1 | BC1L_HUMAN |
| 14 | 403 | 40.0 | 226 | 1 | BC1L_CRILLO |
| 15 | 371 | 36.8 | 204 | 1 | ARI_XENLA |
| 16 | 177.5 | 17.6 | 208 | 1 | BAK_MOUSE |
| 17 | 175 | 17.5 | 211 | 1 | BAK_HUMAN |
| 18 | 173 | 17.2 | 211 | 1 | BAK_HUMAN |
| 19 | 155.5 | 15.4 | 192 | 1 | BAK_MOUSE |
| 20 | 154.5 | 15.3 | 192 | 1 | BAK_MOUSE |
| 21 | 153 | 15.2 | 192 | 1 | BAK_HUMAN |
| 22 | 150 | 14.9 | 280 | 1 | CEB3_MOUSE |
| 23 | 147 | 14.6 | 192 | 1 | BAK_MOUSE |
| 24 | 146.5 | 14.5 | 218 | 1 | BAK_HUMAN |
| 25 | 143 | 14.2 | 177 | 1 | NR13_COTJA |
| 26 | 137.5 | 13.7 | 143 | 1 | BAK_HUMAN |
| 27 | 136.5 | 13.6 | 271 | 1 | CEB3_MOUSE |
| 28 | 118 | 11.7 | 175 | 1 | BC1L_HUMAN |
| 29 | 117 | 11.6 | 194 | 1 | BC1L_HUMAN |
| 30 | 112 | 11.1 | 350 | 1 | WCL1_HUMAN |
| 31 | 105 | 10.4 | 172 | 1 | BC1L_HUMAN |
| 32 | 99.5 | 9.9 | 179 | 1 | EAR_MOUSE |
| 33 | 98.5 | 9.8 | 179 | 1 | EAR_MOUSE |

| | | | | | |
|----|------|-----|------|---|-------------|
| 34 | 98.5 | 9.8 | 179 | 1 | EAR_MOUSE |
| 35 | 87 | 8.6 | 3433 | 1 | POLG_KUNTM |
| 36 | 85.5 | 8.5 | 358 | 1 | GINA_LACSA |
| 37 | 85 | 8.4 | 275 | 1 | DABP_AGRIS |
| 38 | 83.5 | 8.3 | 660 | 1 | SCHEB_BRAVA |
| 39 | 82.5 | 8.2 | 1440 | 1 | POLG_JAEVN |
| 40 | 82.5 | 8.2 | 3432 | 1 | POLG_JAEVN |
| 41 | 80 | 7.9 | 541 | 1 | PTCD_MOUSE |
| 42 | 79.5 | 7.9 | 872 | 1 | STY_STREN |
| 43 | 79.5 | 7.9 | 872 | 1 | STY_STREN |
| 44 | 79 | 7.8 | 396 | 1 | PORA_PYRPU |
| 45 | 79 | 7.8 | 541 | 1 | PTCD_MOUSE |

ALIGNMENTS

RESULT 1
ID BC1M_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2 (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLM OR KIAA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "Bcl-2, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.,
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=22389257; PubMed=12477932;
RA Strussberg R.L., Reinhold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanny U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schneringer A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Promotes cell survival.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC -----
CC EMBL: U59747; AAB09056.1; -.
CC EMBL: D87461; BA19666.1; -.
CC EMBL: BC021198; AAH21198.1; -.
CC HSSP: Q07817; IMAZ.
CC Genew: HGNC:995; BCL2L2.
CC MIM: 601931; -.
CC GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
CC GO: GO:0006916; P:anti-apoptosis; TAS.
CC GO: GO:0007283; P:permatogenesis; TAS.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PSS0062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS0063; BH4_2; 1.
CC KX Apoptosis.
CC FT DOMAIN 9 29 BH4.
CC FT DOMAIN 85 104 BH1.
CC FT DOMAIN 136 151 BH2.
CC SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 100.0%; Score 1007; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,Je-83;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGKYLROKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASAPDTRALVADPVGKYLROKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPMWGLVAFVFGALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPMWGLVAFVFGALCAESVKNKEPVLVG 120
QY 121 QVOEMWVALETRLDWHSQGMAEFTLVGDGLAEARRLRBNWMAVSVTVLGAVAL 180
DB 121 QVOEMWVALETRLDWHSQGMAEFTLVGDGLAEARRLRBNWMAVSVTVLGAVAL 180
QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193
QY 181 GALVTGAFPAK 193
DB 181 GALVTGAFPAK 193

RESULT 2
BCLM MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN BCL2L2 OR BCLM.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.",
RL Oncogene 13:665-675 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/10J; PubMed=9500547;
RX MEDLINE=98160183;
RA Ross A.U., Maynre K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256 (1998).
CC -1- FUNCTION: Promotes cell survival.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and
CC in a wide range of tissues, with highest levels in brain, colon,
CC and salivary gland.
CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC function.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U59746; AAB09056.1; -.
CC EMBL: AF030769; AAB86430.1; -.
CC HSSP: Q07817; IMAZ.
CC MGD: MGI:108052; Bcl2l2.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR002475; BCL2_family.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC PROSITE: PSS0062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PS0063; BH4_2; 1.
CC KX Apoptosis.
CC FT DOMAIN 9 29 BH4.
CC FT DOMAIN 85 104 BH1.
CC FT DOMAIN 136 151 BH2.
CC SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 99.3%; Score 1000; DB 1; Length 193;
Best Local Similarity 99.0%; Pred. No. 4,Je-83;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGKYLROKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
DB 1 MATPASAPDTRALVADPVGKYLROKGYVCGAGPGSPADPLHQARRAGDEFETFRFRT 60
QY 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPMWGLVAFVFGALCAESVKNKEPVLVG 120
DB 61 FSDLAQLHVTGSAQORFTQVSDLEFQGGPMWGLVAFVFGALCAESVKNKEPVLVG 120
```

D6 61 FSDIAQLHTVPPSAQQRFTQVSDLEFQGPMMKSLTVFFVFGALCAESVNKMEPLV 120

QY 121 QVQEMWVAAYETSLADWIMHSSGGMALFTLYGDSGLLEARRLREGNMSVYTVLTGVAL 180

D6 121 QVQDMWVAAYETSLADWIMHSSGGMALFTLYGDSGLLEARRLREGNMSVATVLTGVAL 180

QY 181 GALVTYGAFFPAK 193

D6 181 GALVTYGAFFPAK 193

| RESULT 3 | |
|-----------|-------------|
| ARI_XENLA | |
| ID | ARI_XENLA |
| AC | 091827. |
| STANDARD; | PRT; 228 AA |

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator R1 (XRL) (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxId=8355;
[1]
PP SEQUENCE FROM N.A.
RC TISSUE=Head.
RA MEDLINE=95331613; PubMed=7607538;
RX Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes";
RL Gene 158:171-179(1995).
CC
CC -1- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC
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| | | |
|-----|------------|---|
| DR | HSPB1 | A02462; CMA5; efs.1; . |
| DR | HSPB7 | Q07817; IMA2. |
| DR | InterpC1 | IPR000712; Bc12_BH. |
| DR | InterpG1 | IPR003093; Bc12_BH4. |
| DR | InterpP1 | IPR002475; Bc12_family. |
| DR | Pfam1 | PF00452; Bc1-2; 1. |
| DR | Pfam2 | PF02180; BH4; 1. |
| DR | SMART1 | SM00337; BCL; 1. |
| DR | SMART2 | SM00265; BH4; 1. |
| DR | PROSITE1 | PS01080; BH1; 1. |
| DR | PROSITE2 | PS01258; BH2; 1. |
| DR | PROSITE3 | PS50062; Bc12_FAMILY; 1. |
| KW | Apoptosis; | Transmembrane. |
| XK | NON TER | 1 |
| FT | DOMAIN | 120 .. 139 BH1. |
| FT | DOMAIN | 171 .. 186 BH2. |
| FT | TRANSMEM | 207 .. 227 POTENTIAL. |
| SEQ | SEQUENCE | 228 AA; 25068 MW; C19SD449A5E5F8A9 CRC64; |

| Query Match | 64.23 | Score 646.5 | DB 1 | Length 228 |
|-----------------------|-----------------|-------------------|----------|------------|
| Best Local Similarity | 67.9% | Pred. No. 3.8e-51 | | |
| Matches 125 | Conservative 21 | Mismatches 35 | Indels 3 | Gaps |

10 TRALVDFVGVKQKGYVCGAGPGRAPADLHQAMAAAGDEFETSPRPTFSDLAQH 69

```

Db      48 SRALVEDVLRVYLCCQRLV---PEPSGAASCALHSAPAAADFEERERRQAFSEISTQIH 104
QY      70 VTGSAQCRFTQVSDDELFOGGENMGRLYAFVYFGALCAESVNMKEBPLYQOVENMVAY 129
Db      105 VTGTGYAFAEVAGSLFGQGVNWRITYAFYFGALCAESVNMKEBPLPRIDQNMVTY 164
QY      130 LETRLADWTHSSGGNAEFTALYGDALDEEARLREGNWSAVRYTLTGVALGALVTGAF 189
Db      165 LEINLADWVQSNNGNNGFLTYGDGALIEARQRQEGNWSAKTYLTGAVALGALMTVGAL 224
QY      190 FASK 193
Db      225 FASK 228

```

| RESULT 4 | |
|------------------|-------------|
| BCLX_CHICK | |
| ID_BCLX_CHICK | STANDARD; |
| AC_007816_088808 | PRT; 229 AA |

DT 01-FEB-1995 (Rel. 31, created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
GN Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turkra L.H., Mao X., Nunez G., Thompson C.B.,
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.",
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.,
RT "Differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis",
Mol. Reprod. Dev. 47:26-29(1997).
CC -1-
CC FUNCTION: Dominant regulator of apoptotic cell death. The long
CC form displays cell death repressor activity, whereas the short

```
CC CC
CC -1 SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC CC envelope (By similarity).
CC -1 ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=Long;
CC CC iso14=Q07816-1; Sequence=Displayed;
CC CC Name=Short;
CC CC iso15=Q07816-2; Sequence=VSP_000514;
CC -1 TISSUE SPECIFICITY: Highest expression in organs with lymphoid
CC CC development.
CC -1 DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
CC CC function. Interact BH1 and BH2 domains are required for anti-
CC CC apoptotic activity (By similarity).
CC -1 SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1 SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1 SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1 SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1 SIMILARITY: Belongs to the Bcl-2 family.
```

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CC -----

DR EMBL; 223110; CAA0657.1; -

DR EMBL; U26645; AAB07677.1; -

DR PIR; A47537; A47537.

DR HSSP; P53563; IAF3.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR InterPro; IPR002475; Bcl2_family.

DR InterPro; IPR004725; Bcl2-reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRfam; TIGR00865; bcl-2; 1.

DR PROSITE; PSS0062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1; 1.

DR PROSITE; PS0063; BH4_2; 1.

DR Apoptosis; Transmembrane; Alternative splicing.

FT DOMAIN 4 24 BH4.

FT DOMAIN 82 96 BH3.

FT DOMAIN 125 144 BH1.

FT DOMAIN 176 191 BH2.

FT TRANSMEM 206 223 POTENTIAL.

FT VARSPIC 185 229 ERFVLYGNNAAEELRKQGFENKMLTGATVAGVLLGLSL
LSRK -> VRTALP (in isoform short).
/FTIDVSP 000514.

SO SEQUENCE 229 AA; 25733 MW; A97D3AD04C059DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 7,1e-32;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----VCGAGPGGGP----- 37

DB 6 RELVDFVSYKLSQKCHCSELEEDENRTDAEAMDSVYNGSPSWHPAGHYVNGAT 65

QY 38 -----AADPLHQAARAGDEFEFRFRFTFSDLAQLHTVPGSAQRFTQVSD 85

DB 66 VRRSSLEHVEIVRASVYRQALPDADDEFLRYRAFSDLTSQHLITPGTAQVSFEQVNE 125

QY 86 LFQGGFNWGRVAFVFGAALCAESVYKMEPLVQGVQVWVAVYLETPLADWISSGWA 145

DB 126 LFHDGVNMGRIVAFPSFGALCVESVDKEMRYLVGRIVSWMTTYLTDLHDPWIGNGWE 185

QY 146 EFTALYGDALBARRLRGNWASVRTVYTGVALGALVTGCAFFASK 193

DB 186 RFVDLYGNNA---AAELRKQGFENKMLTGATVAGVLL-IGSLLSRK 229

RESULT 5

BCIX_PIG STANDARD; PRT; 233 AA.

AC 077737;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).

GN BCL2L1 OR BCL2L OR BCIX.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OC NCBI_TaxID=9823;

OX RN

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=99171363; PubMed=10072723;
RA Bartling B., Hoffmann J., Holz J., Schulz R., Heusch G., Darmer D.;
RT "Quantification of cardioprotective gene expression in porcine
short-term hibernating myocardium.";

RL J. Mol. Cell. Cardiol. 31:147-158(1999).

CC -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (By similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC X(L) binds to SIVA isoform 1 (By similarity).

CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).

CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -1- SIMILARITY: Belongs to the Bcl-2 family.

CC -----

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CC -----

DR EMBL; AJ001203; CAA04597.1; -

DR HSSP; Q07817; IMAZ.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR InterPro; IPR002475; BCL2_FAMILY.

DR InterPro; IPR004725; Bcl2-reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRfam; TIGR00865; Bcl-2; 1.

DR PROSITE; PSS0062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1; 1.

DR PROSITE; PS0063; BH4_2; 1.

DR Apoptosis; Mitochondrion; Transmembrane.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

SO SEQUENCE 233 AA; 26061 MW; 18BF6FA041912B2 CRC64;

Query Match 42.9%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. No. 9e-32;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28

DB 6 RELVDFVSYKLSQKCHCSELEEDENRTDAEAMDSVYNGSPSWHPAGHYVNGAT 65

QY 29 CGAGPESGPAA-----PLHQAARAGDEFEFRFRFTFSDLAQLHTVPGSAQRFT 80

DB 66 NGA-TGSSSLDAREVTPMAAVQALRBAGDEFLRYRAFSDLTSQHLITPGTAQVSFE 124

QY 81 QVSDLELFQGGFNWGRVAFVFGAALCAESVYKMEPLVQGVQVWVAVYLETPLADWISS 140

DB 125 QVNLDFRQGVNMGRIVAFPSFGALCVESVDKEMRYLVGRIVSWMTTYLTDLHDPWIG 184

QY 141 SGMNAEFTALYDGALEBEARLRRE--GNWASVRVLTGAVAGAL 183
Db 185 NCGMDTFEYELGNNAAEBSRKGGRFMRFLTGTLAGVLLSL 229

RESULT 6
BCLX_HUMAN STANDARD; PRT; 233 AA.
AC 007817; 092976;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN BCL2L1 OR BCL2L OR BCLX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.,
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death."
RL Cell 74:587-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM X(L)).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Logucliano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.S., McKwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP METAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; PubMed=764501;
RA Sedlak T.W., Oliva Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [5]
RP METAGENESIS OF BHL AND BHZ DOMAINS.
RX MEDLINE=96170038; PubMed=859636;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL."
RL Nature 379:554-556(1996).
RN [6]
RP INTERACTION WITH SIVA.
RX MEDLINE=22008092; PubMed=12011449;
RA Xue L., Chu F., Cheng Y., Sun X., Borthakur A., Ramazao M., Pandey P.,
RA Mu M., Schlossman S.F., Prasad K.V.S.;
RT "Siva-1 binds to and inhibits Bcl-X(L)-mediated protection against UV
RT radiation-induced apoptosis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).
RN [7]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; PubMed=9020082;
RA Sattler M., Liang H., Nettelsheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mittl A.C.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis."
RL Science 275:983-986(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256675; PubMed=8692274;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettelsheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
RT cell death."
RL Nature 381:335-341(1996).
RN [9]
RP CLEAVAGE BY CASPASES, AND METAGENESIS OF ASP-61.
RX MEDLINE=98118550; PubMed=9435230;
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA Takahashi A., Kaetan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-XL through caspase interaction."
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
RN [10]
RP FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
RP apoptotic activity is inhibited by association with SIVA isoform
RP 1. Inhibits activation of caspases (By similarity). Appears to
RP regulate cell death by blocking the voltage-dependent anion
RP channel (VDAC) by binding to it and preventing the release of the
RP caspase activator, cytochrome c, from the mitochondrial membrane.
RP The Bcl-X(S) isoform promotes apoptosis.
RP SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.
RP Heterodimerization with BAX does not seem to be required for anti-
RP apoptotic activity. Isoform Bcl-X(L) binds to SIVA isoform 1.
RP SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
RP envelope (By similarity).
RP ALTERNATIVE PRODUCTS:
RP Event-Alternative splicing; Named isoforms=3;
RP Name=Bcl-X(L); Sequence=Displayed;
RP Name=Bcl-X(S); Sequence=VSP_000515;
RP Name=Bcl-X(beta); Sequence=VSP_000516;
RP Name=Bcl-X(beta); Sequence=VSP_000517;
RP TISSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells
RP that undergo a high rate of turnover, such as developing
RP lymphocytes. In contrast, Bcl-X(L) is found in tissues containing
RP long-lived postmitotic cells, such as adult brain.
RP DOMAIN: The BH4 domain is required for anti-apoptotic activity.
RP The BH1 and BH2 domains are required for both heterodimerization
RP with other Bcl2 family members and for repression of cell death.
RP PIV: Proteolytically cleaved by caspases during apoptosis. The
RP cleaved protein, lacking the BH4 domain, has pro-apoptotic
RP activity.
RP SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
RP SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
RP SIMILARITY: Belongs to the Bcl-2 family.
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CC -----

DR EMBL/ Z23116; CAAB0663.1; -

DR EMBL/ Z23115; CAAB0661.1; -

DR EMBL/ U72398; AAB17384.1; -

DR EMBL/ BC019307; AAB19307.1; -

DR PIR/ B47537; B47537.

DR PIR/ JEO203; JEO203.

DR PDB/ 1BXU; 29-OCT-97.

DR PDB/ 1LXL; 21-APR-97.

DR PDB/ 1MAZ; 21-APR-97.

DR PDB/ 1GSU; 07-FEB-01.

DR PDB/ 1GSM; 21-MAR-01.

DR PDB/ 1GJH; 13-JUN-01.

DR Genew; HGNC.992; BCL2L1.

DR MIM; 600339; -

DR GO; GO:0005739; C:mitochondrion; TAS.

DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.

DR GO; GO:0006916; P:anti-apoptosis; TAS.

DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.

DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR InterPro; IPR002475; Bcl2_family.

DR InterPro; IPR004725; Bcl2_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PSS0062; BCL2_FAMILY; 1.

DR PROSITE; P01080; BH1; 1.

DR PROSITE; P01258; BH2; 1.

DR PROSITE; P01259; BH3; 1.

DR PROSITE; P01260; BH4.1; 1.

DR PROSITE; PSS0063; BH4.2; 1.

KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;

KW 3D-structure.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

FT SITE 61 62 CLEAVAGE (BY CASPASE-1).

FT VARSPLIC 126 188 Missing (in isoform Bcl-X(S)).

FT VARSPLIC 189 233 /Fric=VSP 000515.

FT VARSPLIC 189 233 DTFVELYGNMAAESKRGGRFRNRMFLTGAVVLGSL

FT VARSPLIC 189 233 FSRK -> VTRKPLVCPSELGAGRSPTLLILYFLLCMTI

FT VARSPLIC 189 233 VEDVDS (in isoform Bcl-X(beta)).

FT VARSPLIC 189 233 /Fric=VSP 000516.

FT VARSPLIC 189 233 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY

FT VARSPLIC 189 233 FRD->VRA: NO HETERODIMERIZATION WITH BAX.

FT VARSPLIC 189 233 VNM->AIL: LOSS OF ANTI-APOPTOTIC

FT VARSPLIC 189 233 ACTIVITY.

FT VARSPLIC 189 233 GRI->ELN: LOSS OF ANTI-APOPTOTIC

FT VARSPLIC 189 233 ACTIVITY.

FT VARSPLIC 189 233 MEDLINE=97289584; Pubmed=9144489;

FT VARSPLIC 189 233 Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,

FT VARSPLIC 189 233 Ohta S., Seidlin M.F., Nunez G.;

FT VARSPLIC 189 233 "Genomic organization, promoter region analysis, and chromosome

FT VARSPLIC 189 233 localization of the mouse bcl-x gene.",

FT VARSPLIC 189 233 J. Immunol. 158:4750-4757(1997).

FT VARSPLIC 189 233 -I- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-

FT VARSPLIC 189 233 apoptotic activity is inhibited by association with SIVA isoform

FT VARSPLIC 189 233 1. Inhibits activation of caspases (By similarity). Appears to

FT VARSPLIC 189 233 regulate cell death by blocking the voltage-dependent anion

FT VARSPLIC 189 233 channel (VDAC) by binding to it and preventing the release of the

FT VARSPLIC 189 233 caspase activator, cytochrome c, from the mitochondrial membrane.

FT VARSPLIC 189 233 The Bcl-X(S) isoform promotes apoptosis.

FT VARSPLIC 189 233 -I- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By

FT VARSPLIC 189 233 similarity). Heterodimerization with BAX does not seem to be

FT VARSPLIC 189 233 required for anti-apoptotic activity (By similarity). Isoform Bcl-

FT VARSPLIC 189 233 X(L) binds to Siva isoform 1 (By similarity).

Query Match 42.6%; Score 428.5; DB 1; Length 233;

Best Local Similarity 41.3%; Pred. No. 17e-31;

Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADPVCYKLRQKQY-----V 28

Db 6 RELVVDPLSYKLSQKQYSSQSDVENETEARPEGSEMETPSAINGNPSHLDSPAV 65

QY 29 CGAGPGEAGPAD-----PLHOANRAAGDEFETFRFTPSDLAQLHVTGSAQGRFT 80

Db 66 NGA-TGHSSSIDAREVIMPAAYKALREAGDEFELRYRRAFSDLTSQLHTPGAYQSF 124

QY 81 QVSDLEFGQGNMRLVAFVFGALCAESVNMEMELVQGVQENWAVYLETLPADTHS 140

Db 125 QVVELFRDGVNMGRIYAFSPGALCVESVDKEMQVLVSRIAMWATYINDHLEPIQE 184

QY 141 SGCAEFTALYGDALTEARLRE--GNWASVTVLTGAVALAL 183

Db 165 NGMDTFVELYGNMAAESKRGGRFRNRMFLTGAVVLGSL 229

RESULT 7

BCLX_MOUSE STANDARD; PRT: 233 AA.

AC Q64373; Q60657; Q60658; Q61338;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).

GN BCL2L1 OR BCL2L OR BCLX.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2A4B;

RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).

RC STRAIN=C57BL/6; TISSUE=Brain;

RA MEDLINE=95331139; Pubmed=7607090;

RL Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,

RA Thompson C.B., Nunez G.;

RT "bcl-XL is the major bcl-x mRNA form expressed during murine

RT development and its product localizes to mitochondria.",

RL Development 120:3033-3042(1994).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).

RC TISSUE=Pre-B cell;

RA MEDLINE=95052604; Pubmed=7963517;

RL Fang W., Rivard J.O., Mueller D.L., Behrens T.W.;

RT "Cloning and molecular characterization of mouse bcl-x in B and T

RT lymphocytes.",

RL J. Immunol. 153:4388-4398(1994).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).

RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;

RA MEDLINE=98051053; Pubmed=9390687;

RL Yang X.-F., Weber G.F., Cantor H.;

RT "A novel Bcl-x isoform connected to the T cell receptor regulates

RT apoptosis in T cells.",

RL Immunol. 7:629-639(1997).

RN [5]

RP SEQUENCE FROM N.A.

RC MEDLINE=97289584; Pubmed=9144489;

RA Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,

RA Ohta S., Seidlin M.F., Nunez G.;

RT "Genomic organization, promoter region analysis, and chromosome

RT localization of the mouse bcl-x gene.",

RL J. Immunol. 158:4750-4757(1997).

CC -I- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-

CC apoptotic activity is inhibited by association with SIVA isoform

CC 1. Inhibits activation of caspases (By similarity). Appears to

CC regulate cell death by blocking the voltage-dependent anion

CC channel (VDAC) by binding to it and preventing the release of the

CC caspase activator, cytochrome c, from the mitochondrial membrane.

CC The Bcl-X(S) isoform promotes apoptosis.

CC -I- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By

CC similarity). Heterodimerization with BAX does not seem to be

CC required for anti-apoptotic activity (By similarity). Isoform Bcl-

CC X(L) binds to Siva isoform 1 (By similarity).

CC -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
 CC envelope for Bcl-X(L). Cytoplasmic for Bcl-X(delta-TM).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=BCL-X(L);
 CC IsoId=Q64373-1; Sequence=Displayed;
 CC Name=BCL-X(S);
 CC IsoId=Q64373-2; Sequence=VSP_000517;
 CC Name=BCL-X(beta);
 CC IsoId=Q64373-3; Sequence=VSP_000518;
 CC Name=BCL-X(delta-TM);
 CC IsoId=Q64373-4; Sequence=VSP_000519;
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 CC brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-
 CC TM) expression is enhanced in B and T lymphocytes that have been
 CC activated.
 CC -1- DEVELOPMENTAL STAGE: Bcl-X(beta) is expressed in both embryonal
 CC and postnatal tissues, whereas Bcl-X(L) is predominantly found in
 CC postnatal tissues.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization
 CC with other Bcl2 family members and for repression of cell death.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
 CC apoptotic activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC
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 CC -----
 CC EMBL: X83574; CAAS8557.1; -
 CC EMBL: L35049; AAA51039.1; -
 CC EMBL: L35048; AAA51040.1; -
 CC EMBL: U10102; AAA82174.1; -
 CC EMBL: U10101; AAA82173.1; -
 CC EMBL: U10100; AAA82172.1; -
 CC EMBL: U51279; AAC53460.1; -
 CC EMBL: U78031; AAB96881.1; -
 CC EMBL: U78030; AAB96881.1; JOINED.
 CC PIR: I49055; I49055.
 CC PIR: I49056; I49056.
 CC PIR: I49057; I49057.
 CC HSSP: P53563; IAF3.
 CC MGD: MGI.88139; Bcl2l.
 CC InterPro: IPR000712; Bcl2_BH.
 CC InterPro: IPR003093; Bcl2_BH4.
 CC InterPro: IPR002475; Bcl2_family.
 CC InterPro: IPR004725; Bcl2_reg.
 CC Pfam: PF00452; Bcl2_2; 1.
 CC Pfam: PF02180; BH4_1.
 CC SMART: SM00337; BCL; 1.
 CC SMART: SM00265; BH4; 1.
 CC TIGRFAMs: TIGR00865; bcl-2; 1.
 CC PROSITE: PS50062; BCL2_FAMILY; 1.
 CC PROSITE: PS01080; BH1_1.
 CC PROSITE: PS01258; BH2_1.
 CC PROSITE: PS01259; BH3_1.
 CC PROSITE: PS01260; BH4_1; 1.
 CC PROSITE: PS00063; BH4_2; 1.
 CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
 KW DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.
 FT VARSPPLIC 126 188 Missing (in isoform BCL-X(S)).
 FT VARSPPLIC 189 233 /FTId=VSP_000517.
 FT VARSPPLIC 189 233 DTFVLYGNNAAESRKGQERFNRFLGTAVGVLLGSL
 FT BCL-X(beta).
 FT /FTId=VSP_000518.
 FT VARSPPLIC 194 233 LYGNNAAESRKGQERFNRFLGTAVGVLLGSLFSRK
 FT -> GHDCGMCSAGLTLQSEVTRH (in isoform
 FT BCL-X(delta-TM)).
 FT /FTId=VSP_000519.
 SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;
 Query Match 42.6%; Score 428.5; DB 1; Length 233;
 Best Local Similarity 41.3%; Pred. No. 1.7e-31;
 Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;
 QY 11 RALVADFVGYKLRQGY-----Y 28
 Db 6 RELVDFLSTKLSQKYSWSPDVENRTAPETEARPSAINGNPSMHLADSPAV 65
 QY 29 CGAGPGEQPAD-----PLHQMRAGDEPFRFRPTSPDLAOLHTVPGSAQGRFT 80
 Db 66 NGA-TGHSSSIDAREVITMAAVKQALREAGDEPFLRYRARSDDLTSQHLTPGTAQSE 124
 QY 81 QVSDLEFGCGENWGLVAFVFGAALCAESYKMEPLVGVQCEMVAVYETRLADWTHS 140
 Db 125 QVNNLEFPGDGVNWGRIVAFSFGGALCVESVDKEMQVLSRIASMMATYINDHLEPMIQE 184
 QY 141 SGNAEFLALYDGDALREARLRE--GNWASVRVTLGAVAGL 183
 Db 185 NGMDTFVDLYGNNAAESRKGQERFNRFLGTAVGVLLGSL 229
 RESULT 8
 BCLX RAT STANDARD, PRT, 233 AA.
 ID BCLX RAT PRT, 233 AA.
 AC P53563; P70613; P70614; Q62678; Q62836; Q64087; Q64128;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
 RC TISSUE=Brain;
 RA Michaelidis T.M.;
 RU Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Wesselingh S.L.; David G.L.; Choi S.; Velluona M.; Hardwick J.M.;
 RU Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
 RC TISSUE=Thymus;
 RX MEDLINE=96278736; PubMed=8662675;
 RA Shiraawa N.; Inohara N.; Okada S.; Yuzaki M.; Shoji S.-I.; Ohka S.;
 RT "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
 RT unspliced RNA, promotes apoptosis in promyeloid cells";
 RL J. Biol. Chem. 271:13258-13265 (1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=95128487; PubMed=7828536;
 RA Tilly J.L.; Tilly K.L.; Kenton M.L.; Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive

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RT      bcl-2 and bcl-x-long messenger ribonucleic acid levels." ;
RL      Endocrinology 136:232-241(1995).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX      MEDLINE=98010630; PubMed=9346936;
RA      Artomai M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA      Morikawa K.
RT      "Crystal structure of rat Bcl-XL. Implications for the function of
RT      the Bcl-2 protein family." ;
RL      J. Biol. Chem. 272:27886-27892(1997).
CC      -1- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
CC      apoptotic activity is inhibited by association with SIVA isoform
CC      1. Inhibits activation of caspases (By similarity). Appears to
CC      regulate cell death by blocking the voltage-dependent anion
CC      channel (VDCC) by binding to it and preventing the release of the
CC      caspase activator, cytochrome c, from the mitochondrial membrane.
CC      The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.
CC      -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC      similarity). Heterodimerization with BAX does not seem to be
CC      required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC      X(L) binds to SIVA isoform 1 (By similarity).
CC      -1- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC      envelope (By similarity).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=Bcl-X(L);
CC      IsoId=P53563-1; Sequence=Displayed;
CC      Name=Bcl-X(S);
CC      IsoId=P53563-2; Sequence=VSP_000520;
CC      Name=Bcl-X(beta);
CC      IsoId=P53563-3; Sequence=VSP_000521;
CC      -1- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is
CC      specifically expressed in cerebellum, heart, and thymus. In the
CC      ovary, the predominant form is Bcl-X(L), with a small but
CC      detectable level of Bcl-X(S).
CC      -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC      The BH1 and BH2 domains are required for both heterodimerization
CC      with other Bcl2 family members and for repression of cell death.
CC      -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC      cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC      activity (By similarity).
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      -1- SIMILARITY: Belongs to the Bcl-2 family.
CC      -----
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CC      -----
DR      EMBL; X82537; CAAS7886.1; -
DR      EMBL; X82537; CAAS7887.1; -
DR      EMBL; U10579; AAB19257.1; -
DR      EMBL; U72350; AAB17353.1; -
DR      EMBL; U72349; AAB17352.1; -
DR      EMBL; U34963; AAB77686.1; -
DR      EMBL; S76513; AAC60701.2; ALT_INIT.
DR      EMBL; S78284; AAC60702.1; -
DR      PIR; S517431; S517431.
DR      PIR; S51761; S51761.
DR      PDB; 1AF3; 07-JUL-97.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; Bcl2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.

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| | | | |
|----|--|---|-----|
| DR | SMART; SM00265; BH4; 1. | | |
| DR | TIGRFAWS; TIGR00865; bcl-2; 1. | | |
| DR | PROSITE; PSS0062; BCL2_FAMILY; 1. | | |
| DR | PROSITE; PS01060; BH1; 1. | | |
| DR | PROSITE; PS01258; BH2; 1. | | |
| DR | PROSITE; PS01259; BH3; 1. | | |
| DR | PROSITE; PS01260; BH4; 1. | | |
| DR | PROSITE; PSS0063; BH4_2; 1. | | |
| KW | Apoptosis; Mitochondrion; Alternative splicing; Transmembrane; 3d-structure. | | |
| FT | DOMAIN | 4 | 24 |
| FT | DOMAIN | 86 | 100 |
| FT | DOMAIN | 129 | 148 |
| FT | DOMAIN | 180 | 195 |
| FT | TRANSMEM | 210 | 226 |
| FT | VAASPIC | 126 | 188 |
| FT | VARSPIC | 189 | 233 |
| FT | | | |
| FT | | | |
| FT | CONFLICT | 6 | 6 |
| FT | CONFLICT | 12 | 12 |
| FT | CONFLICT | 64 | 64 |
| FT | CONFLICT | 81 | 81 |
| FT | CONFLICT | 119 | 119 |
| FT | CONFLICT | 143 | 144 |
| FT | CONFLICT | 199 | 199 |
| FT | CONFLICT | 201 | 201 |
| FT | HELIX | 4 | 19 |
| FT | TURN | 20 | 21 |
| FT | TURN | 25 | 28 |
| FT | TURN | 82 | 83 |
| FT | HELIX | 84 | 100 |
| FT | HELIX | 106 | 112 |
| FT | TURN | 116 | 117 |
| FT | HELIX | 120 | 127 |
| FT | HELIX | 128 | 131 |
| FT | TURN | 132 | 133 |
| FT | HELIX | 137 | 156 |
| FT | TURN | 157 | 158 |
| FT | TURN | 160 | 161 |
| FT | HELIX | 162 | 177 |
| FT | TURN | 178 | 178 |
| FT | HELIX | 179 | 184 |
| FT | TURN | 185 | 186 |
| FT | HELIX | 187 | 195 |
| Q | SEQUENCE | 233 AA; 26158 MW; 2862B6C63864BC8F CRC64; | |

| | | | | |
|-----------------------|-------|-------------------|------|----------------------------------|
| Query Match | 42.6% | Score 428.5 | DB 1 | Length 233 |
| Best Local Similarity | 41.3% | Pred. No. 1.7e-31 | | |
| Matches | 93 | Conservative | 22 | Mismatches 57, Indels 53, Gaps 4 |

| | | | | |
|----|-----|---|--------|-----|
| QY | 11 | RALVADFWGYKLRQKGY | -----V | 28 |
| | | | | |
| | | | | |
| Db | 6 | RELIVADFLSYKLSQKGYSMQSPDVEENRTREAPETEPRERETPSAINGNPSMHLADSPAV | | 65 |
| | | | | |
| | | | | |
| QY | 29 | CGAGREGEGAAD-----PLHQMAAGDEDETRPRRFFSLAQQLMHTFGSAQORT | | 80 |
| | | | | |
| | | | | |
| Db | 66 | NGA-TGHSSSDLDAREVTPMAAVKQALREADEDFELRRRAFSDLTSQHLITPGTAYQSE | | 124 |
| | | | | |
| | | | | |
| QY | 81 | QVSDLEFGQGPWRCGLVAFVFGAALCAESVNMEMESLVCQVDEMMVAVLETRLADWIS | | 140 |
| | | | | |
| | | | | |
| Db | 125 | QVYNLEFRGYNWGRIVAFVFGALCVESVDDEMQLVSRISMATYLNHLEPQIE | | 184 |
| | | | | |
| | | | | |
| QY | 141 | SGGMAEFTALYGDGALIEPARRLE--GNMVASVTVLTGAVALGAL | | 183 |
| | | | | |
| | | | | |
| Db | 185 | NGGMDTFVDLYGNMNALESRRKQGERFNRNMLTGMVAVAGVLLGSL | | 229 |
| | | | | |
| | | | | |

| | |
|------------|------------------------|
| RESULT 9 | |
| BCL2_CHICK | STANDARD; PRT; 233 AA. |
| ID | BCL2_CHICK |

AC 000709;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92375724; PubMed=1508712;
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 in a variety of tissues including lymphoid and neuronal organs in
 adult and embryo.";
 RT Nucleic Acids Res. 20:4187-4192(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Casals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 homologue of the Bcl-2 oncoprotein";
 RL Biochim. Biophys. Acta 1132:109-113(1992).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 domains, and is necessary for anti-apoptotic activity (By
 similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 kidney, heart, ovary and brain, with the highest levels in the
 thymus. In the embryo, highly levels expressed in all tissues with
 high levels in the bursa of Fabricius.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 for interaction with RAIF-1 (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, D13382, BAA01978.1, -;
 DR EMBL, D13381, BAA01978.1, JOINED.
 DR EMBL, Z11961, CAAT8018.1, -;
 DR PIR, A37332, A37332.
 DR PIR, S24390, S24390.
 DR HSSP, Q07817, IMAZ.
 DR InterPro, IPR000712, Bcl2_BH.
 DR InterPro, IPR003093, Bcl2_BH4.
 DR InterPro, IPR002475, Bcl2_family.
 DR InterPro, IPR004725, Bcl2_reg.
 DR Pfam, PF00452, Bcl-2, 1.
 DR Pfam, PF02180, BH4, 1.
 DR SMART, SM00337, BCL, 1.

DR SMART, SM00265, BH4, 1.
 DR TIGRPM, TIGR00865, bcl-2, 1.
 DR PROSITE, PS50062, BCL2_FAMILY, 1.
 DR PROSITE, PS01080, BH1, 1.
 DR PROSITE, PS01258, BH2, 1.
 DR PROSITE, PS01259, BH3, 1.
 DR PROSITE, PS01260, BH4, 1.
 DR PROSITE, PS01260, BH4, 1.
 DR PROSITE, PS50063, BH4_2, 1.
 KM Apoptosis, Transmembrane, Mitochondrion.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 87 101 BH3.
 FT DOMAIN 130 149 BH1.
 FT DOMAIN 181 196 BH2.
 FT TRANSMEM 208 228 POTENTIAL.
 FT CONFLICT 64 64 E -> S (IN REF. 2).
 FT CONFLICT 67 82 GSAAAEVPPAGLRP -> ARLLVRCPRRLGCA
 (IN REF. 2).
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB64C3D CRC64;
 Query Match 42.1%; Score 423.5; DB 1; Length 233;
 Best Local Similarity 38.0%; Pred. No. 4; 7e-31;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;
 QY 9 DTRALVADPVGYKLRQKGYVCGAG-----PGSGPADP----- 41
 DB 10 DNRREIVLKTIHYKLSQRGDVAAGEDRPVPAPAPAAVAAGAASHHREPPGSA 69
 QY 42 -----LHQMRAAGDEFEFRFRRTSDLAQLHTVGSAGQRTQSD 84
 DB 70 AASEVPPAGLRPAPPGVHALRQGDDEFSSRYQDRFQMGQLHTFTAGRFVAVE 129
 QY 85 ELFGCGPMMGRILVAFVFGAALCASVVKEMEPVGVQGVMMVYLETRLDMWTHSSGGM 144
 DB 130 ELFRGVGVMMGRVAFVFEFGVGVCSVVRKMSPLVDNIAITMTETLNRLHNMVQDNGM 189
 QY 145 AEFTLYSDGALIEEARLRLEGNMASVRLTGAVALGALVTVGAFPAASK 193
 DB 190 DAFVELYGN-----SWRPPLFDRSWISLKLITLS-LVLVGACITLGAIVLGHK 233
 RESULT 10
 BCL2_BOVIN
 ID BCL2_BOVIN STANDARD; PRT; 229 AA.
 AC 002718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RX MEDLINE=98162580; PubMed=9501056;
 RA Reyes R.A., Cockrell G.L.;
 RT "Increased ratio of bcl-2/bax expression is associated with bovine
 RT leukemia virus-induced leukemogenesis in cattle".
 RL Virology 242:184-192(1998).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1) (By similarity).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2

domains, and is necessary for anti-apoptotic activity. Also
interacts with APAF-1, RAF-1 and p53BP2 (By similarity).
SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
membrane of the nuclear envelope and the endoplasmic reticulum (By
similarity).
-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
for interaction with RAF-1 (By similarity).
-1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
anti-apoptotic activity. Growth factor-stimulated phosphorylation
on Ser-70 by PKC is required for the anti-apoptosis activity and
occurs during the G2/M phase of the cell cycle (By similarity). In
the absence of growth factors, Bcl2 appears to be phosphorylated
by other protein kinases such as ERKs and stress-activated
kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
similarity).
-1- PTM: Proteolytically cleaved by caspases during apoptosis. The
cleaved protein, lacking the BH4 domain, has pro-apoptotic
activity, causes the release of cytochrome c into the cytosol
promoting further caspase activity (By similarity).
-1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
-1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
-1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
-1- SIMILARITY: Belongs to the Bcl-2 family.

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or send an email to license@isb-sib.ch).

DR EMBL: U92434; AAB53319.1; -
DR HSSP: Q07817; 1MAZ.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
KM Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; ADIDDAF99EFPLID CRC64;

Query Match 41.4%; Score 416.5; DB 1; Length 229;
Best Local Similarity 38.2%; Pred. No. 2e-30;
Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;

QY 9 DRRALADVGVYLRKGVYCGAG-----PGP----- 35
DB 10 DNRBEIWKTHYLSRGYEMDAGGAAPGGLSSQPGSTPAPSTSPPPPA 69
QY 36 ---GPAADP---LHQAPRAAGDEFTFRFTFSDLAOLHTVPGSAQGRFQVSDDELFG 88
DB 70 AAGGAPSPVPPVYHLTLRAGDPSRRYRDRDFAEMSSQLHTPLFARERFATVYELFR 129

QY 89 GGNPWGRVAFVFEVGAALCAESVKNENPLVGVQVEMVAVYLETRLADMTSSGGMAEFT 148
DB 130 DGNVWGRVAFVFEVGVWCVESVNRKMSPLVDSIALMWTEYLNRHHTWTLQDNGWDFAV 189
QY 149 ALYEDGALFEARRLRBEGNMAVSRTVLGVALGALVTGVAFFPSK 193
DB 190 ELYG----PSMRPFDPSWLSLKALISIAL-VGACITLGAYLGRK 229

RESULT 11
BCL2_RAT
ID BCL2_RAT STANDARD; PRT; 236 AA.
AC P49950; Q62837; Q64032;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94193015; PubMed=8144041;
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly U.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [3]
RP SEQUENCE OF 19-172 FROM N.A.
RX MEDLINE=95059917; PubMed=7969891;
RA Castren B., Ohga Y., Berzaghi M.P., Tzimasiorgis G., Thoenen H.,
RA Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
including factor-dependent lymphohematopoietic and neural cells.
Regulates cell death by controlling the mitochondrial membrane
permeability. Appears to function in a feedback loop system with
caspases. Inhibits caspase activity either by preventing the
release of cytochrome c from the mitochondria and/or by binding to
the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
domains, and is necessary for anti-apoptotic activity. Also
interacts with APAF-1, RAF-1 and p53BP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
highest levels in reproductive tissues. In the adult brain,
expression is localized in mitral cells of the olfactory bulb,
granule and pyramidal neurons of hippocampus, pontine nuclei,
cerebellar granule neurons, and in ependymal cells. In prenatal
brain, expression is higher and localized in the neuroepithelium
and in the cortical plate.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
anti-apoptotic activity. Growth factor-stimulated phosphorylation
on Ser-70 by PKC is required for the anti-apoptosis activity and

occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).

- P1M: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

- SIMILARITY: Belongs to the Bcl-2 family.

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DR EMBL; U14680; AAA53662.1; -

DR EMBL; U34964; AAA7687.1; -

DR EMBL; S74122; -; NOT_ANNOTATED_CDS.

DR PIR; I53744; I53744.

DR PIR; I57432; I57432.

DR HSSP; Q07817; IMA2.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH4.

DR InterPro; IPR002475; Bcl2_family.

DR InterPro; IPR004725; Bcl2_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BH4; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS00662; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4_1; 1.

DR PROSITE; PS00663; BH4_2; 1.

KM Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD_RES 70 75 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT CONFLICT 42 42 A -> R (IN REF. 2).

FT CONFLICT 157 157 S -> G (IN REF. 1).

FT CONFLICT 164 164 S -> Y (IN REF. 2).

FT CONFLICT 212 212 L -> Q (IN REF. 2).

SC SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query March 41.1%; Score 414; DB 1; Length 236;
Best Local Similarity 36.2%; Pred. No. 3,4e-30;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY DTRALVDFVGYKLRQGY----- 27
Db 10 DNEIIVKVIHYKLSQCYEMDGDSDSAPLRAPPTGIGSFQPSKSRTPAVHRDTAART 69
QY 28 -----VCGAGSGEPAADPLQAMRAAGDEFTRFRRTFSDIAQJHTVPSGAQORFTQ 81
Db 70 SPRLPLVANGPALSPVPVYVHLTLRAGDDFSRRYRBDPAEMSSQJLHLPFAGRFAN 129
QY 82 VSDLEPFGGNGMGLVAFVFGAALCAESVNEKMEPLVGVGVQVMVAIYETRLADITHSS 141
Db 130 VSELEPFDGVNGMGRIVAFEFEGVMCVESYNREMSPLVDNIALMTEYINRHLHTIQON 189

QY 142 GGNABFTALYGDGALAEARLRGNWASRYTLTGAVAGALVWGAFPSK 193
Db 190 GGNDAFVELYG-----PSMRPLDPFSLSTKLSTLAL-VGACITTGAYIGHK 236

RESULT 12
BCL2_MOUSE
ID BCL2_MOUSE STANDARD; PRT; 236 AA.
AC P10417; P10418; 10; Created)
DT 01-MAR-1989 (Rel. 10; Last sequence update)
DT 01-APR-1993 (Rel. 25; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=87187643; PubMed=3032455;
RA Negishi M., Silit E., Kozak C., Tsujimoto Y., Croce C.M.;
RT "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";
RL Cell 49:455-463 (1987).
RN [2]
RP REVISIONS TO 221-222.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192 (1992).
RN [3]
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=97277291; PubMed=9115213;
RA Ito T., Deng X., Carr B., May W.S., Jr.;
RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL J. Biol. Chem. 272:11671-11673 (1997).
RN [4]
RP DEPHOSPHORYLATION BY PP2A.
RX MEDLINE=99069407; PubMed=9852076;
RA Deng X., Ito T., Carr B., Mumby M., May W.S., Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatin 1 is mediated by direct interaction with protein phosphatase 2A.";
RL J. Biol. Chem. 273:34157-34163 (1998).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (Apaf-1).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Interacts with PP58P2 (By similarity). Also interacts with APAF-1 and RAFL-1.
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=P10417-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P10417-2; Sequence=VSP_000513;
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAFL-1.
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation

on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A).

PM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

Similarity: Contains 1 Bcl-2 homology 1 (BH1) domain.

Similarity: Contains 1 Bcl-2 homology 2 (BH2) domain.

Similarity: Contains 1 Bcl-2 homology 3 (BH3) domain.

Similarity: Contains 1 Bcl-2 homology 4 (BH4) domain.

Similarity: Belongs to the Bcl-2 family.

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EMBL: L31532; AAA37282.1; -

EMBL: M16506; AAA37282.1; JOINED.

EMBL: M16506; AAA37281.1; -

PIR: B25960; TVNSBL.

HSSP: Q07817; IMAZ.

MGI: MGI:88138; Bcl2.

GO: GO:0005829; C:cytosol; IDA.

GO: GO:0008189; F:apoptosis inhibitor activity; IDA.

GO: GO:0005515; F:protein binding; IPI.

GO: GO:0006915; P:apoptosis; IDA.

InterPro: IPR000712; Bcl2 BH.

InterPro: IPR003093; Bcl2 BH4.

InterPro: IPR004475; Bcl2 family.

InterPro: IPR004725; Bcl2_reg.

Pfam: PF00452; Bcl-2; 1.

Pfam: PF02180; BH4; 1.

SMART: SMO0337; BCL; 1.

SMART: SMO0265; BH4; 1.

TIGRfam: TIGR00865; bcl-2; 1.

PROSITE: PS00562; BCL2_FAMILY; 1.

PROSITE: PS01080; BH1; 1.

PROSITE: PS01258; BH2; 1.

PROSITE: PS01259; BH3; 1.

PROSITE: PS01260; BH4; 1.

PROSITE: PS00653; BH4_2; 1.

Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD RES 70 70 PHOSPHORYLATION (BY PKC).

FT VARSLIC 193 236 DAFVELYGRSMRPLPFSLSKLTSLALVACITLGAYL.

GRK -> VEGALVE (in isoform Beta).

Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

FT SEQUENCE 236 AA; 26425 MW; AAB5EF6B0766B0A CRC64; /FTID=VSP 000511.

Query Match 41.0%; Score 413; DB 1; Length 236;

Best Local Similarity 37.5%; Pred. No. 4.2e-30;

Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADPVGYLARKGYVCGAG-----PG----- 34

DB 10 DREIMTKIHYLSRGYEMDADADAPLGAAPPGFSGFSPSNPMVAHREMAART 69

QY 35 -----EGPADP-----LHOAKRAGDEFEFRRTESDLAQLAHLVTPGSAQGRFTQ 81

DB 70 SPURPVATAGPALSPVPCVHLTLRRAGDDFSRRYRDRFAMSSQLHLPFTAGRPAT 129

QY 82 VSDLPFGGPNWGLVAFVFGAALCAESYKNEKEDLVGOYQEMVAYLETSLADWTHSS 141

DB 130 VVEELFRDGVNMGRIIVAFEFEGVWCVESVREMSPLVDNIALMTETYLNRHLATWIQDN 189

QY 142 GGMDEFTALYDGDALDEERRRREGNMASVPTVLTGVALGALTVAGVAFPSK 193

DB 190 GGMDFVELYIG-----PSMRPLPFSWLSLTSLAL-VGACITLGAYLGRK 236

RESULT 13

BCL2_HUMAN

ID BCL2_HUMAN STANDARD; PRT; 239 AA.

AC P10415; P10416; Q13842; Q16197;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).

RX MEDLINE=86259760; PubMed=3523487;

RA Tsujimoto Y., Croce C.M.;

RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma."

RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).

RN [2]

RP REVISIONS TO 96; 110 AND 237.

RX MEDLINE=92375724; PubMed=1508712;

RA Ebnuchi Y., Ewert D.L., Tsujimoto Y.;

RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo."

RL Nucleic Acids Res. 20:4187-4192(1992).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RX MEDLINE=87002488; PubMed=2875799;

RA Cleary M.L., Smith S.D., Sklar J.;

RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation."

RL Cell 47:19-28(1986).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RX MEDLINE=86196071; PubMed=2834197;

RA Seto M., Jaeger U., Hockett R.D., Grantinger W., Bennett S.;

RA Goldman P., Korsmeyer S.J.;

RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-1g fusion gene in lymphoma."

RL EMBO J. 7:123-131(1988).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.

RX MEDLINE=87002488; PubMed=2875799;

RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schachwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RC TISSUE=Testis;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stempelen M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Rata S.S., Loguettano N.A., Peters G.J., Abramson R.D., Millary S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
 RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
 RX MEDLINE=92096610; PubMed=1339299;
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.,
 RT "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 RN [8]
 RP SUBCELLULAR LOCATION.
 RP MEDLINE=91066924; PubMed=2250705;
 RX Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.,
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 RN [9]
 RP MUTAGENESIS.
 RP MEDLINE=94239528; PubMed=8183370;
 RX Yin X.-M., Oltvai Z.N., Korsmeyer S.J.,
 RT "Bhl and Bh2 domains of Bcl-2 are required for inhibition of
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 RN [10]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
 RX MEDLINE=98057466; PubMed=9395403;
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kasstan M.B., Bedi A.,
 RA Ueno K., Hardwick J.M.,
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
 RL Science 278:1966-1968(1997).
 RN [11]
 RP INTERACTION WITH TP53BP2.
 RX MEDLINE=96251339; PubMed=8668206;
 RA Naumovski L., Cleary M.L.,
 RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes
 RT cell cycle progression at G2/M.";
 RL Mol. Cell. Biol. 16:3884-3892(1996).
 RN [12]
 RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE=21260650; PubMed=11368354;
 RA Ruvoilo P.P., Deng X., May W.S.,
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
 RL Leukemia 15:515-522(2001).
 RN [13]
 RP PHOSPHORYLATION BY ASK1/JNK1.
 RX MEDLINE=20036804; PubMed=10565752;
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.,
 RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
 RT protein kinase pathway normally activated at G(2)/M.";
 RL Mol. Cell. Biol. 19:8469-8478(1999).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact Bhl and Bh2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1, Raf-1 and TP53BP2.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intercellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=PI0415-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=PI0415-2; Sequence=VSP_000512;
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The Bh4 domain is required for anti-apoptotic activity and
 CC for interaction with Raf-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the Bh4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
 CC II chronic lymphatic leukemia) by a chromosomal translocation
 CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
 CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
 CC the chromosomal translocation could be attributed to the Ig
 CC somatic hypermutation mechanism resulting in nucleotide
 CC transitions.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: Belongs to the Bcl-2 family.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.html".
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 CC
 CC EMBL, M13994; AAA51813.1; ALT_SEQ.
 CC EMBL, M13995; AAA51814.1; ALT_SEQ.
 CC EMBL, M14745; AAA35581.1;
 CC EMBL, X06467; CAA29778.1;
 CC EMBL, AY220759; AA026045.1;
 CC EMBL, BC027258; AA027258.1;
 CC EMBL, S72602; AAD14111.1; ALT_SEQ.
 CC PIR, B29409; TVHBI1.
 CC PIR, C37332; TVHBI1.
 CC PDB, 1G5W; 2I-JUN-01.
 CC PDB, 1G7H; 13-JUN-01.
 CC Genew; HGNC:990; BCL2.
 CC MIM: 151430; -;
 CC GO, GO:0005743; C:mitochondrial inner membrane; TAS.
 CC GO, GO:0008189; F:apoptosis inhibitor activity; TAS.
 CC GO, GO:0006916; P:anti-apoptosis; TAS.
 CC GO, GO:0006959; P:humoral immune response; TAS.
 CC GO, GO:0008285; P:negative regulation of cell proliferation; TAS.
 CC GO, GO:0000074; P:regulation of cell cycle; TAS.
 CC InterPro, IPR007012; Bcl2_BH.
 CC InterPro, IPR003093; Bcl2_BH4.
 CC InterPro, IPR002475; Bcl2_family.
 CC InterPro, IPR004725; Bcl2_reg.
 CC
 CC Query Match 41.0%; Score 412.5; DB 1; Length 239;
 CC Best Local Similarity 37.0%; Pred. No. 4.7e-30;
 CC Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;
 CC
 CC 9 DTPALVADFGVYKLRQKGYVCGAG-----PGE----- 35

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Db      10 DNEIWKYIHYKLSQGYEMDAGVGAAPGAAPAGIFSSQPGHTPPAASRDPAVART 69
Qy      36 -----GPAADP-----LHQAMRAGDEFEFRFRFRFSDLAQHTPPSAOQR 78
Db      70 SPLQTPAAGAAAGPALSPVPVAVHLLTKQAGDFSRFRYRDRPAEMSOLHTLPTFARGR 129
Qy      79 FTQVSDLEFGGPNMGRILVAFVFGAALCAESYKXEMEPVQGVQVQVMMVAYLETRLADWI 138
Db      130 FAVVVELFRDGVNWKIRIVAFVFGVGVVCSYVNSPLVDNIALMTEYINRLHHTWI 189
Qy      139 HSGGMAEFTALYGDGALBEARPLREGNNAVTVITGVALGALVTGAFPAASK 193
Db      190 QDNGWDPAFVELYGV-----PSMRPLFPDSWLSKTLISLAL-VGACITTLGAYLGKH 239

RESULT 14
BCL2_CR1LO
ID      BCL2_CR1LO      STANDARD;      PRT;      236 AA.
AC      09JUT8;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Apoptosis regulator Bcl-2.
GN      BCL2.
OS      Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Cricetulus.
OX      NCBI_TaxID=10030;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Ovary; PubMed=10973819;
RA      MEDLINE=20431763;
RX      Tomicic M.T., Kaina B.;
RT      "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT      protein.";
RL      Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN      [2]
RP      SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX      MEDLINE=21092839; PubMed=11181062;
RT      Tomicic M.T., Kaina B.;
RT      "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT      and caspase-3.";
RL      Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC      -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC      including caspase-dependent lymphohematopoietic and neural cells.
CC      Regulates cell death by controlling the mitochondrial membrane
CC      permeability. Appears to function in a feedback loop system with
CC      caspases. Inhibits caspase activity either by preventing the
CC      release of cytochrome c from the mitochondria and/or by binding to
CC      the apoptosis-activating factor (APAF-1) (By similarity).
CC      -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK, BAK and
CC      BCL-X(L). Heterodimerization with BAX requires intact BH1 and BH2
CC      domains, and is necessary for anti-apoptotic activity. Also
CC      interacts with APAF-1, RAF-1 and TP53BP2 (By similarity).
CC      -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC      membrane of the nuclear envelope and the endoplasmic reticulum.
CC      -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC      for interaction with RAF-1 (By similarity).
CC      -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC      anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC      on Ser-70 by PKC is required for the anti-apoptosis activity and
CC      occurs during the G2/M phase of the cell cycle (By similarity). In
CC      the absence of growth factors, Bcl2 appears to be phosphorylated
CC      by other protein kinases such as ERKs and stress-activated kinases
CC      (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC      (By similarity).
CC      -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC      cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC      activity, causes the release of cytochrome c into the cytosol
CC      promoting further caspase activity.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

```

```

CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      -1- SIMILARITY: Belongs to the Bcl-2 family.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AJ271720; CAB92245.1; -.
DR      PIR; J07383; J07383.
DR      HSSP; Q07817; IMAZ.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; Bcl2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.
DR      SMART; SM00265; BH4; 1.
DR      TIGRFAMs; TIGR00865; bcl-2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01256; BH2; 1.
DR      PROSITE; PS01259; BH3; 1.
DR      PROSITE; PS01260; BH4_1; 1.
DR      PROSITE; PS01260; BH4_2; 1.
DR      PROSITE; PS50063; BH4_2; 1.
KW      Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT      DOMAIN 10..30 BH4.
FT      DOMAIN 90..104 BH3.
FT      DOMAIN 133..152 BH1.
FT      DOMAIN 184..199 BH2.
FT      TRANSMEM 209..230 POTENTIAL.
FT      SITE 64..65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT      MOD_RES 70..70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ      SEQUENCE 236 AA; 26491 MW; BECADFLIEF337228 CRC64;

Query Match      40.0%; Score 403; DB 1; Length 236;
Best local similarity 35.3%; Pred. No. 3.4e-29;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

Qy      9 DTRALVADPFGYKLRQKY-----
Db      10 DNEIWKYIHYKLSQGYEMDAGVGAAPGAAPAGIFSSQPGHTPPAASRDPAVART 69
Qy      28 -----VCGAGPGEPAADPLHQAMRAGDEFEFRFRFRFSDLAQHTPPSAOQRFTQ 81
Db      70 SPLRPIVATGPTLSPVPVAVHLLTKRAGDFSRFRYRDRPAEMSOLHTLPTFARGRFAR 129
Qy      82 VSDDLFGGPNMGRILVAFVFGAALCAESYKXEMEPVQGVQVQVMMVAYLETRLADWIHSS 141
Db      130 FAVVVELFRDGVNWKIRIVAFVFGVGVVCSYVNSPLVDNIALMTEYINRLHHTWIQDN 189
Qy      142 GGMAEFTALYGDGALBEARPLREGNNAVTVITGVALGALVTGAFPAASK 193
Db      190 QDNGWDPAFVELYGV-----PSVRPLFPDSWLSKTLISLAL-VGACITTLGAYLGKH 236

RESULT 15
AR11_XENLA
ID      AR11_XENLA      STANDARD;      PRT;      204 AA.
AC      091828;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Apoptosis regulator Bcl (XR11).
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC      Xenopodinae; Xenopus.

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=9531613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RL cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: Confers strong protection against cell death.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: Developmental regulation occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82461; CA57844.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 101..120 BH1.
FT DOMAIN 152..167 BH2.
FT TRANSMEM 181..198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFCB65DDA4CA03 CRC64;

Query Match 36.8%; Score 371; DB 1; Length 204;
Best Local Similarity 42.1%; Pred. No. 2.2e-26;
Matches 82; Conservative 25; Mismatches 62; Indels 26; Gaps 4;

QY 10 TRALVADPVGVKLRQKGYVC-----GAGPGEGRPADPLHQAKR 47
DB 5 SRDLVEKVFVSKKLSQ-NEACRKFSNNENPNPYLMEPSISERPEGATOGIVEEVLQALL 63
QY 48 AAGDEFEFTRRRRTFSDLAQLHTPGSAQORFTQVSDPLFOGQPNWGRILVAFVFGALC 107
DB 64 EATGEFEFLRYQRAFSDLTSQLHTQDPAQSFQVWGEFLFRDSTNWRIVAFPSFRAIC 123
QY 108 AESYKMEPLVQGVQVQVEMVAYLETRLADWIISSGGWAETALYGDGALEARRIRE--G 165
DB 124 VESANKEMTDLLPRIVQMNVNLEHTLQPMWQNGGWEAVGLYGKAAAGSRSGERFG 183
QY 166 NMA5VRTVLTGAVALL 180
DB 184 RLITI-VMLTGVFAL 197

```

Search completed: March 25, 2004, 15:43:01
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:36:20 ; Search time 14 Seconds

(without alignments)
1326.069 Million cell updates/sec

Title: US-09-155-327g-7

Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFGV.....LTGAVALGALVTGAFPSAK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 428.5 | 42.6 | 233 | 2 | bcl-x long - mouse |
| 2 | 428.5 | 42.6 | 233 | 2 | apoptosis regulato |
| 3 | 424.5 | 42.2 | 233 | 2 | BCL-X protein - ra |
| 4 | 423.5 | 42.1 | 233 | 2 | transforming prote |
| 5 | 414 | 41.1 | 232 | 2 | S24390 |
| 6 | 412.5 | 41.0 | 239 | 1 | TVHUA1 |
| 7 | 412 | 40.9 | 236 | 2 | transforming prote |
| 8 | 407 | 40.4 | 236 | 2 | BCL-2 - rat (fragm |
| 9 | 406 | 40.3 | 236 | 1 | TVMSA1 |
| 10 | 404.5 | 40.2 | 233 | 2 | 167431 |
| 11 | 403 | 40.0 | 236 | 2 | JC7383 |
| 12 | 378 | 37.5 | 190 | 2 | A47537 |
| 13 | 377.5 | 37.5 | 214 | 2 | I49057 |
| 14 | 375.5 | 37.3 | 227 | 2 | JE0203 |
| 15 | 356 | 35.4 | 216 | 2 | B37332 |
| 16 | 349.5 | 34.7 | 199 | 1 | TVMSB1 |
| 17 | 346 | 34.4 | 205 | 1 | TVHUB1 |
| 18 | 277.5 | 27.6 | 154 | 2 | I58194 |
| 19 | 182 | 18.1 | 170 | 2 | I49055 |
| 20 | 176 | 17.5 | 211 | 2 | S58875 |
| 21 | 174 | 17.3 | 176 | 2 | I67435 |
| 22 | 173 | 17.2 | 211 | 2 | S58875 |
| 23 | 157.5 | 15.6 | 192 | 2 | D47538 |
| 24 | 153 | 15.2 | 192 | 2 | A47538 |
| 25 | 150 | 14.9 | 261 | 2 | H88578 |
| 26 | 149.5 | 14.8 | 280 | 2 | A53189 |
| 27 | 149.5 | 14.8 | 133 | 2 | I53295 |
| 28 | 146.5 | 14.5 | 179 | 2 | JC7255 |
| 29 | 146.5 | 14.5 | 218 | 2 | B47538 |

30 143 14.2 177 2 S54778
31 141 14.0 255 2 JC7567
32 137.5 13.7 143 2 I18921
33 118 11.7 175 2 I19055
34 112 11.1 350 2 A47476
35 105 10.4 172 2 I49449
36 91.5 9.1 301 2 T36534
37 89 8.8 185 2 B83217
38 87 8.6 343 1 GNWVXV
39 85 8.4 270 2 A12598
40 85 8.4 279 2 B97381
41 84.5 8.4 358 1 A1LCOB
42 83 8.2 417 2 T39939
43 82.5 8.2 1440 1 GNWVJF
44 82.5 8.2 3432 1 GNWVJF
45 81.5 8.1 354 2 S52040

NR-13 protein - qu
Mcl-1a protein - z
bcl-2-associated p
Bcl-2 related - hu
Bcl2 homolog MCL1
hemopoietic-specif
probable lipase/s
hypothetical prote
genome polypeptid
dihydrodipicolinat
glutamate-ammonta
DNA binding protei
genome polypeptid
genome polypeptid
Gln 1.1 protein -

ALIGNMENTS

RESULT 1
149056
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: I49056; S52866
R: Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J: Immunol. 153, 4388-4398, 1994
A: Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A: Reference number: I49055; MUID: 95052604; PMID: 7963517
A: Accession: I49056
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-233 <RES>
A: Cross-references: EMBL:U0101; NID: 9506647; PIDN: AAA82173.1; PID: 9506648
R: Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A: Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu
A: Reference number: S52866
A: Accession: S52866
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-233 <KAM>
A: Cross-references: EMBL: X83574; NID: 9695622; PIDN: CAA58557.1; PID: 9695623
C: Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.9e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 PALVADFYGYLRKQGY-----V 28
DB 6 RELVDFLSYKLSQKGSWSQSPDVENRTEAPEETEARETPEASINGNSWMLADSPAV 65
QY 29 CGAGGGEPSAD-----PIHQMAAGDEFTRRRPSDIAAQLHTVPSAQRFT 80
DB 66 NGA-TGHSLSLDADEVTPMAAVKQALREAGDEFELRRFRAVSDTISQHTTPGAYVSFE 124
QY 81 QVSDLEFCGSPNMGRLVAFVFGAALCAESVKNMEPLVGVGVQVEMVAYLETRLDADYHS 140
DB 125 QVAVELPFDGVNMGRIYAFVFGAALCVESVDKMNQVLSRISAMATYINDHLEPIQGE 184
QY 141 SGGAAEFTALYGDALREARLRE--GNMASVRLTGAVALGAL 183
DB 185 NGMDTFVDLYGNNAALASRKQGERFNRFLTGMTVAGVLLGSL 229

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N: Alternate names: bcl-2-related protein
N: Contains: apoptosis regulator bcl-xS

C/Species: Homo sapiens (man)
 C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
 C/Accession: B47537, C47537
 R/Boise, L.H.; Gonzalez-Garcia, M.; Poetema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
 Cell 74, 597-608, 1993
 A/Title: bcl-1, a bcl-2-related gene that functions as a dominant regulator of apoptotic
 A/Reference number: A47537; MID:93364977; PMID:8358789
 A/Accession: B47537
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-233 <B01>
 A/Cross-references: GB:L20121; MID:9510900; PIDN:CAA80661.1; PID:9510901
 A/Accession: C47537
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-65; G, 71-125, 189-233 <B02>
 A/Cross-references: GB:L20122; MID:9623236; PIDN:CAA80662.1; PID:9623237
 C/Genetics:
 A/Gene: GDB:BCL2L
 A/Cross-references: GDB:228079
 C/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: alternative splicing; apoptosis
 F:1-233/Product: apoptosis regulator bcl-XL #status predicted <MAT>
 F:1-125,189-233/Product: apoptosis regulator bcl-XS #status predicted <MA2>

Query Match 42.6%; Score 428.5; DB 2; Length 233;
 Best Local Similarity 40.6%; Pred. No. 2.9e-32;
 Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

11 RLVDVFGYKLRQGY-----VCAGP-----GEGPAA 39
 6 RLVDVFLYSKQSGVSWQPSDVEENRTAPEGTEBEMTPSAINGNPSMHLADSPAV 65
 40 D-----PLHQMPAAGDEFEFRRTFSDLAQLHVTGSAQGRFTQ 81
 66 NGATAHSSLDAREVTPMAAVKQALREAGDEFELRYRAFSLTLSQHLITGTAAQSEFQ 125
 82 VSDLPFGGPMGRVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSS 141
 126 VVNEFLFRDGVNMGRIYAFVFGAALCVESVDKEMQVLSRIAMWATYLNHLDEPWIGEN 165

QY 142 GMAEFTALYDGALEBARLRE--GNWASVRYTLGAVAGAL 183
 DB 186 GMDTFVLYGNMAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3
 S51761
 BCL-X protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 28-Jul-2003
 C/Accession: S51761, S51762
 R/Michaelidis, T.M.
 Submitted to the EMBL Data Library, November 1994
 A/Reference number: S51761
 A/Accession: S51761
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-223 <MIC>
 A/Cross-references: EMBL:X82337; NID:9607176; PIDN:CAA57886.1; PID:9607177
 A/Experimental source: embryonic; brain
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-125,189-233 <MT2>
 A/Cross-references: EMBL:X82337; NID:9607176; PIDN:CAA57887.1; PID:9607178
 A/Experimental source: embryonic; brain
 A/Note: smaller form due to splicing
 C/Genetics:
 A/Introns: 125/3
 C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.2%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 6.7e-32;
 Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 13 LVNDFYGYKLRQGY-----VCAGP-----GEGPAA 39
 DB 8 LVNDFYGYKLRQGY-----VCAGP-----GEGPAA 39
 QY 31 AGPEGPAA-----PLHQMPAAGDEFEFRRTFSDLAQLHVTGSAQGRFTQ 82
 DB 68 A-TGHSSLDAREVTPMAAVKQALREAGDEFELRYRAFSLTLSQHLITGTAAQSEFQ 126
 QY 83 SDELFGGPMGRVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSSG 142
 DB 127 VVNEFLFRDGVNMGRIYAFVFGAALCVESVDKEMQVLSRIAMWATYLNHLDEPWIGEN 186

QY 143 GMAEFTALYDGALEBARLRE--GNWASVRYTLGAVAGAL 183
 DB 187 GMDTFVLYGNMAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4
 A37332
 transforming protein (bcl-2-alpha) - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
 C/Accession: A37332; S35453
 R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari-
 A/Reference number: A37332; MID:9235724; PMID:1508712
 A/Accession: A37332
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-233 <EGU>
 A/Cross-references: EMBL:D11381
 C/Genetics:
 A/Introns: 189/3
 C/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.1%; Score 423.5; DB 2; Length 233;
 Best Local Similarity 38.0%; Pred. No. 8.3e-32;
 Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;

9 DTRLVADVFGYKLRQGYVCGAG-----GEGPAA-----GEGPAA 41
 10 DNRSLVLYKTYHYLSQRYDMAAGEDRPVPAPAPAAVAAAGASSHRRPEPPSA 69
 42 -----LHQMPAAGDEFEFRRTFSDLAQLHVTGSAQGRFTQ 84
 DB 70 AASEVPAEGLRPAPEGVHLALRQADDEFRRYQDFQNSQHLITPTAQRFAVVE 129
 QY 85 ELFGGPMGRVAFVFGAALCAESVKNEMEPVGVQVQEMWVAYLETRLADWTHSSG 144
 DB 130 ELFRDGVNMGRIYAFVFGAALCVESVDKEMQVLSRIAMWATYLNHLDEPWIGEN 189

QY 145 AEFTALYDGALEBARLREGNWASVRYTLGAVAGALVTVGAFPAASK 193
 DB 190 DAFVELYGN---SNRPLDFPMSISLKITLS-LVVGACITTGAYIGHK 233

RESULT 5
 S24390
 transforming protein (bcl-2) homolog - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 28-Jul-2003
 C/Accession: S24390
 R/Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
 Biochim. Biophys. Acta 1137, 109-113, 1992
 A/Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
 A/Reference number: S24390; MID:92379084; PMID:1511008
 A/Accession: S24390
 A/Status: preliminary

A.Molecule type: mRNA
 A.Residues: 1-232 <CAZ>
 A.Cross-references: EMBL:Z11961; NID:G62969; PIRN:CAA78018.1; PID:G62970
 C/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: mitochondrion; transmembrane protein

Query Match 41.1%; Score 414; DB 2; Length 232;
 Best Local Similarity 37.7%; Pred. No. 6.3e-31;
 Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADVFVGYLROKGYCCAG-----PGEGRADP----- 41
 Db 10 DNRREIVKXIHXYLSORGYEMADGVDGAPPAAPGIFSSQPGHTPHAPASRDPAART 69
 QY 42 -----LHQAMRAAGDEFEFRPRRTSDLAOLHTVPGSAQRFTQVAD 85
 Db 70 LTVRCPLRGCAAPGVHIALRQAGDEFRRYQRFPAQMSQDLHTLPFATGRFVAAYVE 129
 QY 86 LFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGVQVEMVAYLETRLADWISSGGMA 145
 Db 130 LFRDGNWVRIVAFVFGVGVCMVESVNRKMSPLVDNIAATMTREYLNRLHMTIQDNGMD 189
 QY 146 EFTALYGDGALBEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 AFVEIYLG-----SMRPLFDPSWISLKTILSL-VGVACITLGAYLGHK 232

RESULT 6

Transferring protein bcl-2, splice form alpha - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1986 #sequence revision 07-Jun-1996 #text change 28-Jul-2003
 C/Accession: C37332; A29409; S02452; A24428; A27622; B27622
 R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992

A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A/Reference number: A37332; MUID:92275724; PMID:1508712
 A/Accession: C37332
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: DNA
 A.Residues: 1-239 <EGU>
 A/Note: this report is a correction
 R/Tsujimoto, Y.; Croce, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A>Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for the B-cell lymphoma cell line
 A/Reference number: A29409; MUID:86259760; PMID:3523487
 A/Accession: A29409
 A/Molecule type: mRNA
 A.Residues: 1-95 'A', 97-109 'G', 111-236 'S', 238-239 <TSU>
 A.Cross-references: GB:M1394; NID:9179366; PIRN:AAA5183.1; PID:9179367
 A/Note: this sequence has been corrected in reference A37332
 R/Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
 EMBO J. 7, 123-131, 1988

A>Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene
 A/Reference number: S02452; MUID:88196071; PMID:2834197
 A/Accession: S02452
 A/Molecule type: mRNA
 A.Residues: 1-239 <SET>
 R/Cleary, M.L.; Smith, S.D.; Sklar, J.
 Cell 47, 19-28, 1986
 A>Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer
 A/Reference number: A24428; MUID:87002488; PMID:2875799
 A/Accession: A24428
 A/Molecule type: mRNA
 A.Residues: 1-58 'T', 60-116 'R', 118-239 <CLE>
 A.Cross-references: GB:M14745; NID:9179370; PIRN:AAA5591.1; PID:9179371
 R/Hu, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.
 Oncogene Res. 2, 263-275, 1988

A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: a study of 100 cases
 A/Reference number: A27622; MUID:88217344; PMID:3285301
 A/Accession: A27622
 A/Molecule type: mRNA
 A.Residues: 1-58 'T', 60-239 <HUA>

A/Accession: B27622
 A.Molecule type: DNA
 A.Residues: 1-6 'S', 8-58 'T', 60-128 'C', 130-239 <HUA>
 A/Note: the sequence was determined from the germ-line gene
 C/Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
 C/Genetics:
 A/Genes: GDB:BCL2
 A/Cross-references: GDB:119031; OMIM:151430
 A/Map position: 18q21.3-18q21.3
 C/Function:
 A/Description: blocks apoptosis in hematopoietic cells
 C/Superfamily: bcl apoptosis regulator, inhibitory type
 C/Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 41.0%; Score 412.5; DB 1; Length 239;
 Best Local Similarity 37.0%; Pred. No. 9e-31;
 Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADVFVGYLROKGYCCAG-----PGE----- 35
 Db 10 DNRREIVKXIHXYLSORGYEMADGVDGAPPAAPGIFSSQPGHTPHAPASRDPAART 69
 QY 36 -----GPADP-----LHQAMRAAGDEFEFRPRRTSDLAOLHTVPGSAQR 78
 Db 70 SPLTPAPAPGAPALSPVPVHLTLRQAGDFSRIRDRPAEMSSQDLHTPFARGR 129
 QY 79 FTQVDELFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGVQVEMVAYLETRLADW 138
 Db 130 FATVEELFRDGNWVRIVAFVFGVGVCMVESVNRKMSPLVDNIAATMTREYLNRLHMTIQ 189
 QY 139 HSSGMAEFTALYGDGALBEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 QDNGMDAFVLYG-----PSMRPLFDPSWISLKTILSLAL-VGACITLGAYLGHK 239

RESULT 7

BCL-2 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 28-Jul-2003
 C/Accession: I67432
 R/Tilly, U.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995

A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
 constitutive bcl-2 and bcl-2-long messenger ribonucleic acid levels.
 A/Reference number: I53295; MUID:95129487; PMID:7828536
 A/Accession: I67432
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A.Residues: 1-236 <RES>
 A/Cross-references: EMBL:U34964; NID:91004378; PIRN:AAA77687.1; PID:91004379
 C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.9%; Score 412; DB 2; Length 236;
 Best Local Similarity 36.2%; Pred. No. 9.8e-31;
 Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADVFVGYLROKGY-----PGE----- 27
 Db 10 DNRREIVKXIHXYLSORGYEMDGTGDSAPLRAPPGIFSSQPGESNRTPAVARDTAART 69
 QY 28 -----VCGAGPEGPAAPPLQAMAAAGDEFRRRTFSDLAOLHTVPGSAQRFTQ 81
 Db 70 SPLRPLVANAAPALSPVPVHLTLRQAGDFSRIRDRPAEMSSQDLHTPFARGRFAT 129
 QY 82 VSDLELFGGPNMGRILVAFVFGAALCAESVNMKEPPLVGVQVEMVAYLETRLADWISS 141
 Db 130 VYELFRDGNWVRIVAFVFGVGVCMVESVNRKMSPLVDNIAATMTREYLNRLHMTIQD 189
 QY 142 GMAEFTALYGDGALBEARLRGNMNASVTVLTGAVALGALVTGAFPAASK 193
 Db 190 GGDVAFVLYG-----PSMRPLFDPSWISQSLTILSLAL-VGACITLGAYLGHK 236

A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-214 <RES>
A/Cross-references: EMBL:U10102; NID:G506649; PIDN:AAA2174.1; PID:G506650
C/Genetics:
A/Gene: bcl-x-long
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.8%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 6,7e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADPFYKLRKQGY-----V 27
DB 10 DNRIRVWKYIHYKLSQRGYEMVDVDAAPLGAAPRPGIFSFPESNPTPRAVRDMAART 69
QY 28 -----VCGAGGEGPADPLHQMRRAAGDEFETFRFRFTSDLAOLHTVPGSAOQRF 81
DB 70 SPLRPIVATTQPTLSPVPVVALTLRAGDPSRRIRRDPAEMSSQDLHTPTARGRFAT 129
QY 82 VSDELFOGGRPWGRLVAFVFGAALCAESYVKNEMEPVGVQOEMWVAYLETRLADWIHS 141
DB 130 VVELFDFDGVNMGRIVAFERGVGVKVESVNRKMSPLVDNIALMMEYLRHILHTWICDN 189
QY 142 GGMALFTALYGDGALAEARLRREGNMAVTRVLTGAVALALVTVGAFFASK 193
DB 190 GGMDFAFELYG-----PSVRPLDFPSMLSLKTLISAL-VGACITLGYLGHK 236

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C/Species: Gallus gallus (chicken)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C/Accession: A47537
R/Bolise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A/Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A/Reference number: A47537; MUID:93364977; PMID:8358789
A/Accession: A47537
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-190 <RES>
A/Cross-references: GB:J23110; GB:L20120; NID:G510898; PIDN:CAA0657.1; PID:G510899
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 1.1e-27;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;

QY 11 RALVADPFYKLRKQGY-----VCGAGGEGP----- 37
DB 6 RELVIDFVSYKLSQRGHGWSELEEDENRTDTAAEAMDSVLNGSPWHPAGVNVGAT 65
QY 38 -----AADPLHQMRRAAGDEFETFRFRFTSDLAOLHTVPGSAOQRF 85
DB 66 VHRSSLEVHEIVRASDVRAQIRDADEFELIRRAFSDLTSQHLITPGTVQSFQVNE 125
QY 86 LFOGGRPWGRLVAFVFGAALCAESYVKNEMEPVGVQOEMWVAYLETRLADWIHS 145
DB 126 LPHGVNMGRIVAFERGVGVKVESVNRKMSPLVDNIALMMEYLRHILHTWICDN 185
QY 146 EFTAL 150
DB 186 R-TAL 189

RESULT 13

149057
bcl-x transmembrane deleted - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C/Accession: 149057
R/Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A/Reference number: 149055; MUID:9505604; PMID:7963517

A/Accession: 149057
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-214 <RES>
A/Cross-references: EMBL:U10102; NID:G506649; PIDN:AAA2174.1; PID:G506650
C/Genetics:
A/Gene: bcl-x-long
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 1.4e-27;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;

QY 11 RALVADPFYKLRKQGY-----V 28
DB 6 RELVDFLSYKLSQKYSWSQFSDVENRTAPERTAEARETPSAINGNPSMHLADSPAV 65
QY 29 CGAGGEGPAD-----PLHQMRRAAGDEFETFRFRFTSDLAOLHTVPGSAOQRF 80
DB 66 NGA-TGHSSLDAREVITMAAVKQALREAGDEFELIRRAFSDLTSQHLITPGTVQSF 124
QY 81 QVSDELFOGGRPWGRLVAFVFGAALCAESYVKNEMEPVGVQOEMWVAYLETRLADWIHS 140
DB 125 QVNNLEFDFDGVNMGRIVAFERGVGVKVESVNRKMSPLVDNIALMMEYLRHILHTWICDN 184
QY 141 SGMALFTALYGDGALAEARLRREGNMAVTRVLTGAVALALVTVGAFFASK 193
DB 185 NGMDPTF 191

RESULT 14

JEB0203
apoptosis regulator bcl-x isoform - human
N/Alternate names: h-bcl-xbeta
C/Species: Homo sapiens (man)
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
C/Accession: JEB0203
R/Ban, J.; Bokhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A/Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A/Reference number: JEB0203; MUID:98340865; PMID:9675101
A/Accession: JEB0203
A/Molecule type: mRNA
A/Residues: 1-227 <BAN>
A/Cross-references: GB:U72398; NID:G1622940; PIDN:AAH17354.1; PID:G1622941
C/Genetics:
A/Gene: bcl-x
A/Map position: 20
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.3%; Score 375.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 2.3e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

QY 11 RALVADPFYKLRKQGY-----V 28
DB 6 RELVDFLSYKLSQKYSWSQFSDVENRTAPERTAEARETPSAINGNPSMHLADSPAV 65
QY 29 CGAGGEGPAD-----PLHQMRRAAGDEFETFRFRFTSDLAOLHTVPGSAOQRF 80
DB 66 NGA-TGHSSLDAREVITMAAVKQALREAGDEFELIRRAFSDLTSQHLITPGTVQSF 124
QY 81 QVSDELFOGGRPWGRLVAFVFGAALCAESYVKNEMEPVGVQOEMWVAYLETRLADWIHS 140
DB 125 QVNNLEFDFDGVNMGRIVAFERGVGVKVESVNRKMSPLVDNIALMMEYLRHILHTWICDN 184
QY 141 SGMALFTALYGDGALAEARLRREGNMAVTRVLTGAVALALVTVGAFFASK 193
DB 185 NGMDPTF 191

RESULT 15

B37332

transforming protein (bcl-2-beta) - chicken

C/Species: Gallus gallus (chicken)

C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003

C/Accession: B37332; S35452

R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A/Reference number: A37332; MUID:92375724; PMID:1508712

A/Accession: B37332

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-216 <ESU>

A/Cross-references: EMBL:D11381; EMBL:D11382

C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 35.4%; Score 356; DB 2; Length 216;

Best Local Similarity 38.4%; Pred. No. 1,4e-25;

Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps 2;

QY 9 DTRALVADFYGYKLRQKGYVCGAG-----PGECPADP----- 41

Db 10 DNRKIVLKTHYKLSQKGYDMAAGBDRPPVPAPAPAPAAVAAGASSHRRPEPPGSA 69

QY 42 -----LHQMRRAAGDEFEFRRTFSDLAQLHTYTPGSAOQRFTOVSD 84

Db 70 AASEVPPAEGLRAPRPPGVHLLRQAGDEFRRYQRDPAGMSQGLHTPTAHGRFVAAYE 129

QY 85 ELFGGPNMGRLLVAFYFGAALCAESYNKEMEPVGVQVQEMWVAYLETRLADMIHSSGSA 144

Db 130 ELFRDGVNMGRIYVAFYFGVCMCVESYNREMSPLVDNIATWTEYLNRLHNWIQDNGSM 189

QY 145 AEFT 149

Db 190 VRACA 194

Search completed: March 25, 2004, 15:45:06
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 15:19:05 ; Search time 51 Seconds
(without alignments)
1069.248 Million cell updates/sec

Title: US-09-155-327G-7

Perfect score: 1007
Sequence: 1 MATPAPAPDTRALVADRVG.....LTGAVAGALVTYGAFFAPSK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Geneseqp1360s:*
2: Geneseqp1930s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1007 | 100.0 | 193 | 2 | AA05530 |
| 2 | 1007 | 100.0 | 193 | 7 | ADDA6742 |
| 3 | 1002 | 99.5 | 193 | 2 | AAW61392 |
| 4 | 1002 | 99.5 | 193 | 2 | AAW61392 |
| 5 | 1000 | 99.3 | 193 | 2 | AAW61392 |
| 6 | 1000 | 99.3 | 193 | 2 | AAW61392 |
| 7 | 1000 | 99.3 | 193 | 2 | AAW61392 |
| 8 | 997 | 98.9 | 193 | 2 | AAW61392 |
| 9 | 996 | 98.9 | 193 | 2 | AAW61392 |
| 10 | 996 | 98.9 | 193 | 2 | AAW61392 |
| 11 | 991 | 98.4 | 192 | 2 | AAW61392 |
| 12 | 958.5 | 95.2 | 192 | 2 | AAW61392 |
| 13 | 867 | 86.1 | 166 | 5 | AAW61392 |
| 14 | 821.5 | 81.6 | 166 | 5 | AAW61392 |
| 15 | 766 | 76.1 | 166 | 5 | AAW61392 |
| 16 | 766 | 76.1 | 166 | 5 | AAW61392 |
| 17 | 766 | 76.1 | 166 | 5 | AAW61392 |
| 18 | 433.5 | 43.0 | 411 | 5 | AAW61392 |
| 19 | 431.5 | 42.9 | 411 | 5 | AAW61392 |
| 20 | 428.5 | 42.6 | 233 | 2 | AAW61392 |
| 21 | 428.5 | 42.6 | 233 | 2 | AAW61392 |
| 22 | 428.5 | 42.6 | 233 | 2 | AAW61392 |
| 23 | 428.5 | 42.6 | 233 | 2 | AAW61392 |
| 24 | 428.5 | 42.6 | 233 | 2 | AAW61392 |
| 25 | 428.5 | 42.6 | 233 | 2 | AAW61392 |

| | | | | | | | |
|----|-------|------|-----|---|----------|----------|--------------------|
| 25 | 428.5 | 42.6 | 233 | 4 | AAW61392 | AAW73303 | Rat wild- |
| 27 | 428.5 | 42.6 | 233 | 4 | AAW61392 | AAW64262 | AAW64262 Human Bcl |
| 28 | 428.5 | 42.6 | 233 | 4 | AAW61392 | AAW47515 | AAW47515 Protein e |
| 29 | 428.5 | 42.6 | 233 | 7 | AAW61392 | AAW62921 | AAW62921 Rat Prote |
| 30 | 428.5 | 42.6 | 233 | 7 | AAW61392 | AAW62493 | AAW62493 Human Pro |
| 31 | 428.5 | 42.6 | 233 | 7 | AAW61392 | AAW62491 | AAW62491 Rat Prote |
| 32 | 428.5 | 42.6 | 236 | 6 | AAW61392 | AAW83558 | AAW83558 Tola-BCL |
| 33 | 428.5 | 42.6 | 348 | 6 | AAW61392 | AAW83557 | AAW83557 Tola-BCL |
| 34 | 425 | 42.2 | 225 | 2 | AAW19396 | AAW19396 | AAW19396 "Deprenyl |
| 35 | 424.5 | 42.2 | 233 | 4 | AAW73304 | AAW73304 | AAW73304 Mutant ra |
| 36 | 416.5 | 41.4 | 239 | 4 | AAW64037 | AAW64037 | AAW64037 Human Bcl |
| 37 | 415.5 | 41.3 | 152 | 6 | AAW79760 | AAW79760 | AAW79760 Bcl-XL. 4 |
| 38 | 413 | 41.0 | 236 | 4 | AAW35131 | AAW35131 | AAW35131 Murine Bc |
| 39 | 413 | 41.0 | 236 | 5 | AAW76554 | AAW76554 | AAW76554 Murine Bc |
| 40 | 412.5 | 41.0 | 239 | 2 | AAW87810 | AAW87810 | AAW87810 A human B |
| 41 | 412.5 | 41.0 | 239 | 4 | AAW35130 | AAW35130 | AAW35130 Human Bcl |
| 42 | 412.5 | 41.0 | 239 | 4 | AAW74127 | AAW74127 | AAW74127 Human bcl |
| 43 | 412.5 | 41.0 | 239 | 5 | AAW78479 | AAW78479 | AAW78479 Human Bcl |
| 44 | 412.5 | 41.0 | 239 | 5 | AAW78478 | AAW78478 | AAW78478 Human Bcl |
| 45 | 412.5 | 41.0 | 239 | 5 | AAW76553 | AAW76553 | AAW76553 Human Bcl |

ALIGNMENTS

RESULT 1
AA05530
AA05530 standard; protein; 193 AA.

AC AA05530;
DT 05-JUL-1999 (first entry)
DE Human Bcl-w protein essential for spermatogenesis.
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; 98WO-AU000764.
PR 16-SEP-1997; 97AU-00009228.
PS (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PY Cory S, Adams J, Print C, Gibson L, Koentgen F,
XX WPI; 1999-243890/20.
XX N-PSDB; AA05532.
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
XX Claim 2; Page 33; 52pp; English.
XX The present sequence is human Bcl-w, a pro-survival member of the Bcl-2
XX family which is widely expressed and which is essential for
XX spermatogenesis. The invention relates generally to a method of treatment
XX and to an animal model for the identification of molecules and genetic
XX sequences useful for inducing or reducing fertility of male animals.
XX Methods are provided for the treatment of infertility, or for reducing
XX fertility, by modulating spermatogenesis. An animal model carries a
XX mutation in at least one allele of the human or murine bcl-w gene (see
XX disorganised seminiferous tubules and are substantially infertile, but
XX possess no other major abnormalities as determined by histological
XX examination. They can be used to screen for therapeutic molecules
XX inducing genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 1007; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAPGEGPADPLHQAARAAGDEFEFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAPGEGPADPLHQAARAAGDEFEFRRT 60
QY 61 FSDLAQAQHTVTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
DB 61 FSDLAQAQHTVTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
QY 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWASVRYTLTGAVALL 180
DB 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWASVRYTLTGAVALL 180
QY 181 GALVTGAFPPASK 193
DB 181 GALVTGAFPPASK 193

RESULT 2
ADD6742
ID ADD6742 standard; protein; 193 AA.

XX ADD6742;
AC
XX 29-JAN-2004 (first entry)
DE Human Protein Q92843, SEQ ID NO 12427.
XX
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.

XX WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.
DR GENBANK; Q92843.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 193 AA;
Query Match 100.0%; Score 1007; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 1,4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAPGEGPADPLHQAARAAGDEFEFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAPGEGPADPLHQAARAAGDEFEFRRT 60
QY 61 FSDLAQAQHTVTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
DB 61 FSDLAQAQHTVTPGSAQGRFTQVSDLEFQGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
QY 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWASVRYTLTGAVALL 180
DB 121 QVQEMWVAYLETRLADWTHSSGWAFFETALYGDALBEARLRREGWASVRYTLTGAVALL 180
QY 181 GALVTGAFPPASK 193
DB 181 GALVTGAFPPASK 193

RESULT 3

AAW61392
ID AAW61392 standard; protein; 193 AA.

XX AAW61392;

XX 02-OCT-1998 (first entry)

XX Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-00798897.

XX 23-FEB-1996; 96US-0012201P.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI, 1998-446079/38.
DR N-PSDB; AAV28334.

XX Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.

DR WPI, 1997-489635/45.
 DR N-PSDB; AAY96577.
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 XX
 PS Claim 6; Page 48; 86pp; English.
 CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
 CC -2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases; degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.
 CC Up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators
 CC
 SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
 Best Local Similarity 99.0%; Pred. No. 8.3e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFFTRFRRT 60
 DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFFTRFRRT 60
 QY 61 FSDLAQLHVTPTGSAQQRFTQVSDLPFGGPNMGRVLAFFVGAALCAESVKNKEBPLVG 120
 DB 61 FSDLAQLHVTPTGSAQQRFTQVSDLPFGGPNMGRVLAFFVGAALCAESVKNKEBPLVG 120
 QY 121 QVQEMWVAVLETRLDWTHSSGMAEFTALYGDGALAEARRLRGNWASVTVTLTGAVAL 180
 DB 121 QVQEMWVAVLETRLDWTHSSGMAEFTALYGDGALAEARRLRGNWASVTVTLTGAVAL 180
 QY 181 GALVTVGAFPAK 193
 DB 181 GALVTVGAFPAK 193

RESULT 6
 AAY05532
 ID AAY05532 standard; protein; 193 AA.
 AC AAY05532;
 DT 05-JUL-1999 (first entry)
 DE Human Bcl-w protein essential for spermatogenesis.
 XX
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 XX animal model.
 OS Homo sapiens.
 XX
 XX WO9913710-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX 16-SEP-1998; 98WO-AU000764.
 XX
 XX 16-SEP-1997; 97AU-00009228.
 XX
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 XX WPI, 1999-243890/20.
 XX
 XX N-PSDB; AAX25134.
 DR

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 XX
 XX Disclosure; Page 37; 52pp; English.
 XX

CC The present sequence is described of a derivative of human Bcl-w (see
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 2; Length 193;
 Best Local Similarity 99.0%; Pred. No. 8.3e-102;
 Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFFTRFRRT 60
 DB 1 MATPASAPDTRALVADFGYKLRQKGYCGAGPGGPAADPLHQMRAAGDEFFTRFRRT 60
 QY 61 FSDLAQLHVTPTGSAQQRFTQVSDLPFGGPNMGRVLAFFVGAALCAESVKNKEBPLVG 120
 DB 61 FSDLAQLHVTPTGSAQQRFTQVSDLPFGGPNMGRVLAFFVGAALCAESVKNKEBPLVG 120
 QY 121 QVQEMWVAVLETRLDWTHSSGMAEFTALYGDGALAEARRLRGNWASVTVTLTGAVAL 180
 DB 121 QVQEMWVAVLETRLDWTHSSGMAEFTALYGDGALAEARRLRGNWASVTVTLTGAVAL 180
 QY 181 GALVTVGAFPAK 193
 DB 181 GALVTVGAFPAK 193

RESULT 7
 AAY05531
 ID AAY05531 standard; protein; 193 AA.
 AC AAY05531;
 DT 05-JUL-1999 (first entry)
 DE Mouse Bcl-w protein essential for spermatogenesis.
 XX
 XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 XX animal model.
 OS Mus sp.
 XX
 XX WO9913710-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX 16-SEP-1998; 98WO-AU000764.
 XX
 XX 16-SEP-1997; 97AU-00009228.
 XX
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;
 XX WPI, 1999-243890/20.
 XX

DR N-PSDB; AAX25133.
XX An animal model exhibiting reduced levels of a bcl-w protein and/or
PT protein associated with bcl-w.
XX
XX
PS Claim 2; Page 35; 52pp; English.
XX
CC The present sequence is mouse bcl-w, a pro-survival member of the bcl-2
CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation in at least one allele of the human or murine bcl-w gene (see
CC AAX25133-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;
Query Match 99.3%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 8.3e-102;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTPASAPDTRALVADPFGYKLRQGYVCGAGPBGPAADPLHQMRAAGDEFTRRRRT 60
DB 1 MTPASAPDTRALVADPFGYKLRQGYVCGAGPBGPAADPLHQMRAAGDEFTRRRRT 60
QY 61 FSDLAAGLHTVTPGSAOQRTQVSDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVG 120
DB 61 FSDLAAGLHTVTPGSAOQRTQVSDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVG 120
QY 121 VOEWNVAVYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
DB 121 VOEWNVAVYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193
RESULT 8
AAM97394
ID AAM97394 standard; protein; 192 AA.
XX
AC AAM97394;
XX
DT 20-MAY-1999 (first entry)
XX
DE Mammalian bcl-y protein.
XX
KW Rat bcl-y protein; Bcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Mammalia.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.

XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
PS Claim 2; Col 19-22; 26pp; English.
XX
CC The present sequence represents a mammalian bcl-y protein. The
CC specification describes rat bcl-y protein (Bcl-y) and human bcl-y
CC protein (Hbcl-y). Bcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Bcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Bcl-y and Hbcl-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites
XX
SQ Sequence 192 AA;
Query Match 99.0%; Score 997; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 1.8e-101;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATPASAPDTRALVADPFGYKLRQGYVCGAGPBGPAADPLHQMRAAGDEFTRRRRT 61
DB 1 ATPASAPDTRALVADPFGYKLRQGYVCGAGPBGPAADPLHQMRAAGDEFTRRRRT 60
QY 62 SDLAAGLHTVTPGSAOQRTQVSDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVGQ 121
DB 61 SDLAAGLHTVTPGSAOQRTQVSDELFOGSPNMGRLVAFVFGALCAESVNKMEPLVGQ 120
QY 122 VOEWNVAVYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 181
DB 122 VOEWNVAVYLETRLDWVHSSGMAEFTLYGDGALBEARLRREGNMAVRYTLTGAVALG 180
QY 182 ALVTGAFPAASK 193
DB 181 ALVTGAFPAASK 192
RESULT 9
AAM61391
ID AAM61391 standard; protein; 193 AA.
XX
AC AAM61391;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y protein.
XX
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PR 11-FEB-1997; 97US-00798897.

KM premature cell death; cell death stimulator; prolonged cell life span;
 KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

OS Unidentified.

PN US5883229-A.

PD 16-MAR-1999.

PF 25-NOV-1997; 97US-00978523.

PR 23-FEB-1996; 96US-0012201P.

PR 11-FEB-1997; 97US-00798897.

XX (COCR-) COCENSYS INC.

PI Guastella G.

DR WPI; 1999-214150/18.

PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
 PT modulating programmed cell death.

PS Disclosure; Col 19-20; 26pp; English.

XX The specification describes rat bcl-y protein (rbcl-y) and human bcl-y
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
 CC thought to be involved in programmed cell death (apoptosis and necrosis).
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
 CC with a disruption of the cell death pathway. If they act as cell death
 CC inhibitors, they may be used in therapies to treat subjects suffering
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
 CC degenerative diseases (especially multiple sclerosis), myocardial
 CC infection, vitally induced cell death, aging, spinal cord injuries and
 CC amyotrophic lateral sclerosis - conditions where cells under go premature
 CC cell death as a result of triggers which may or may not be apparent. They
 CC may also be used in this way to develop cell lines which remain viable in
 CC culture for an extended period. In contrast, if they act as cell death
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
 CC cause cell death in, and hence control, parasites

XX Sequence 192 AA;

Query Match 98.4%; Score 991; DB 2; Length 192;

Best Local Similarity 98.4%; Pred. No. 8.1e-101;

Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 61
 DB 1 ATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 QY 62 SLLAAGLHTVTPGSAQGRFTQVSDELFGGPNNGRLVAFVFGAALCAESVNMKEPELVG 121
 DB 61 SLLAAGLHTVTPGSAQGRFTQVSDELFGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 QY 122 VQEMWAVIYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVALG 181
 DB 121 VQDMWVYIETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVALG 180
 QY 182 ALVTVGAFPAK 193
 DB 181 ALVTVGAFPAK 192

RESULT 12
 ID AAY05533
 AC AAY05533 standard; protein; 192 AA.
 XX AAY05533;
 XX DT 05-JUL-1999 (first entry)

XX Mouse Bcl-w protein derivative.

XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
 XX animal model.

OS Mus sp.

PN M09913710-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-AU000764.

PR 16-SEP-1997; 97AU-00009228.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PI Cory S, Adams J, Print C, Gibson L, Koentgen F;

DR WPI; 1999-243890/20.

DR N-PSDB; AAX25135.

PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.

PS Disclosure; Page 39; 52pp; English.

XX The present sequence is described of a derivative of mouse Bcl-w (see
 CC also AAY05533), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The derivative
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates
 CC generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation in at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility

XX Sequence 192 AA;

Query Match 95.2%; Score 958.5; DB 2; Length 192;

Best Local Similarity 94.8%; Pred. No. 3.1e-97;

Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 DB 1 MPTPASAPDTRALVADVGVYKLRQKGYVCGAGGEGPADPLHQAARAGDEFTFRRT 60
 QY 61 FSDLAAGLHTVTPGSAQGRFTQVSDELFGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 DB 61 FSDLAAGLHTVTPGSAQGRFTQVSDELFGGPNNGRLVAFVFGAALCAESVNMKEPELVG 120
 QY 121 QVQEMWAVIYETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVAL 180
 DB 121 QVQDMWVYIETRLADVIHSSGGMAEFTALYDGALEEARLRBGNWASRYTLTGAVAL 179
 QY 181 GALVTVGAFPAK 193
 DB 180 GALVTVGAFPAK 192

RESULT 13
 ID AAW36048
 AC AAW36048 standard; protein; 168 AA.
 XX AAW36048;
 XX AC AAW36048;

XX 22-APR-1998 (first entry)
 XX Mouse bcl-w protein.
 DE Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 XX diagnosis; degenerative disease.
 KW Mus sp.
 XX MO9735971-A1.
 XX 02-OCT-1997.
 XX 27-MAR-1997; 97MO-AU000139.
 XX 27-MAR-1996; 96AU-00008965.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Cory S, Adams JM, Gibson LM, Holmgreen SP;
 PI MPI, 1997-489635/45.
 DR N-PSDB; AAT96578.
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 XX Claim 6; Page 50-51; 86pp; English.
 PS This sequence represents a novel protein, bcl-w, encoded by the mouse bcl
 XX -2 gene family. This gene promotes cell survival, so its modulation is
 CC useful in treatment of cancer or auto-immune diseases, degenerative
 CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
 CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
 CC or in cell transplants. Up-regulation of the gene can also be used to
 CC modify cell lines cultured in vivo, e.g. to develop new lines, to
 CC facilitate isolation of hybridomas and to increase survival of primary
 CC explants during genetic modification. It can be used to produce
 CC recombinant Bcl-w for therapy, diagnosis, antibody production or
 CC screening of potential modulators
 CC
 XX Sequence 168 AA:
 SO
 Query Match 86.1%; Score 867; DB 2; Length 168;
 Best Local Similarity 95.8%; Pred. No. 3.3e-87;
 Matches 161; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MATPASAPDTRALVADPVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 DB 1 MPTPASPTDTRALVADPVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 QY 61 FSDLAQLHTVPGSAOQRFQVSDDELFOGQPNMGRVAFVFGAALCAESVNKEMEPV 120
 DB 61 FSDLAQLHTVPGSAOQRFQVSDDELFOGQPNMGRVAFVFGAALCAESVNKEMEPV 120
 QY 121 QVOEMVAVLETRLADWIHSSGWAFFETALYGDGALAEARLRREGNWA 168
 DB 121 QVOEMVAVLETRLADWIHSSGWAFFETALYGDGALAEARLRREGNWA 168
 RESULT 14
 ID AAO18223 standard; protein; 190 AA.
 XX AAO18223;
 AC AAO18223;
 XX 18-SEP-2002 (first entry)
 DT Human Bcl-Rambo BHO domain related protein #4.
 DE Human; apoptotic signal transduction protein; Bcl-Rambo; BHO domain;
 KW

KW cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
 KW neurotropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
 KW immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
 KW Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
 KW graft versus host disease; autoimmune disease.
 XX Unidentified.
 XX WO200248353-A2.
 XX 20-JUN-2002.
 XX 12-DEC-2001; 2001WO-EP014597.
 XX 12-DEC-2000; 2000DE-01061766.
 XX 04-JAN-2001; 2001DE-01000280.
 XX (APOT-) APOTECH RES & DEV LTD.
 XX Tschoopp J, Hofmann K;
 PI MPI, 2002-537627/57.
 DR New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and
 PT for identifying therapeutic modulators of Bcl-Rambo function.
 PT
 XX Disclosure; Fig 1; 61pp; German.
 PS The present invention provides the protein and coding sequences of the
 CC human Bcl-Rambo apoptotic transcription factor, particularly the BHO
 CC domain. The sequences are useful in the treatment of diseases caused by
 CC incorrectly regulated intracellular signal transduction, including
 CC cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's
 CC diseases), muscular dystrophy, viral infections (including human
 CC immunodeficiency virus), autoimmune disease, septic shock, graft versus
 CC host disease and acute hepatitis. The present sequence is a protein
 CC described in the exemplification of the invention
 CC
 XX Sequence 190 AA:
 SO
 Query Match 81.6%; Score 821.5; DB 5; Length 190;
 Best Local Similarity 88.1%; Pred. No. 4.1e-82;
 Matches 170; Conservative 0; Mismatches 20; Indels 3; Gaps 3;
 QY 1 MATPASAPDTRALVADPVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 DB 1 MATPASAPDTRALVADPVGKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETFRRT 60
 QY 61 FSDLAQLHTVPGSAOQRFQVSDDELFOGQPNMGRVAFVFGAALCAESVNKEMEPV 120
 DB 59 FSDLAQLHTVPGSAOQRFQVSDDELFOGQPNMGRVAFVFGAALCAESVNKEMEPV 118
 QY 121 QVOEMVAVLETRLADWIHSSGWAFFETALYGDGALAEARLRREGNWA 180
 DB 119 QVOEMVAVLETRLADWIHSSGWAFFETALYGDGALAEARLRREGNWA 177
 QY 181 GALVTVGAFVASK 193
 DB 178 GALVTVGAFVASK 190
 RESULT 15
 ID AAM59884 standard; protein; 365 AA.
 XX AAM59884;
 AC AAM59884;
 XX 20-NOV-1998 (first entry)
 DT Amino acid sequence of the cDNA clone Bcl-1like (HAICH29).
 DE Bcl-1like (HAICH29); chronic inflammatory disease; allergic reaction;
 KW immunological disorder; autoimmune disease; anti-infectious agent.
 KW

XX Homo sapiens.
 OS
 XX NO9831800-A2.
 PN
 XX 23-JUL-1998.
 PD
 XX 21-JAN-1998; 98WO-US000960.
 PF
 XX 21-JAN-1997; 97US-0034204P.
 PR 21-JAN-1997; 97US-0034205P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (AUCK-) AUCKLAND UNISERVICES LTD.
 XX
 XX NI J, Rosen CA, Gentz RL, Feng P, Krasanssen GW, Su JY;
 PI
 XX WPI; 1998-414099/35.
 DR N-PSDB; AAV41925.
 DR
 XX
 XX New isolated polynucleotides and encoded polypeptides - used to develop
 PT products for treating e.g. inflammatory diseases, infections,
 PT immunological disorders, autoimmune diseases, allergies or tumours.
 XX
 XX Claim 1; Fig 12A-12D; 120pp; English.
 PS
 XX
 CC This is the amino acid sequence of the cDNA clone Bcl-1ike (HAICH29),
 CC used in the method of the invention. The products of the clone can be
 CC used for treating conditions associated with abnormal expression of the
 CC polypeptides. They can be used for e.g. treating chronic inflammatory
 CC diseases, immunological disorders, autoimmune diseases, inflammatory
 CC diseases, various allergies, and as anti-infectious agents. The products
 CC can also be used for detection and diagnosis
 CC
 XX
 XX Sequence 365 AA;
 SQ

Search completed: March 25, 2004, 15:42:28
 Job time : 52 secs

Query Match 76.1%; Score 766; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.3e-75;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADPVGKLRQKGYVCAGPGSPADPLHOMRAAGDEFFETRRRT 60
 DB 1 MATPASAPDTRALVADPVGKLRQKGYVCAGPGSPADPLHOMRAAGDEFFETRRRT 60
 QY 61 FSDLAAGLHVTTPGSAQORFTQVSDELFOGGPNWGRVAFVFGALCAESVNKEMEPLVG 120
 DB 61 FSDLAAGLHVTTPGSAQORFTQVSDELFOGGPNWGRVAFVFGALCAESVNKEMEPLVG 120
 QY 121 QVOEMWVAVLETRLADWIHSSGM 144
 DB 121 QVOEMWVAVLETRLADWIHSSGM 144

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OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:18:04 ; Search time 2267.1 Seconds

(without alignment)
7652.923 Million cell updates/sec

Title: US-09-155-327g-8

Perfect score: 581

Sequence: 1 atgcgcagccccagcctcaac.....gccttttctgtagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_escba:*
2: em_escbm:*
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4: em_escmu:*
5: em_escro:*
6: em_escpl:*
7: em_escro:*
8: em_escro:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc4:*
13: gb_esc5:*
14: gb_esc6:*
15: em_escfun:*
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28: gb_esc1:*
29: gb_esc2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 560.2 | 96.4 | 582 | 29 | AY421022 Mus muscu |
| 2 | 560.2 | 96.4 | 1949 | 11 | AK015644 Mus muscu |
| 3 | 560.2 | 96.4 | 3487 | 13 | AK004680 Mus muscu |
| 4 | 558.6 | 96.1 | 969 | 13 | BY715200 BY715200 |

| | | | | | | |
|----|-------|------|------|----|----------|--------------------|
| 5 | 503.6 | 86.7 | 967 | 13 | BU503850 | BU503850 AGENCOURT |
| 6 | 501 | 86.2 | 582 | 29 | AY421020 | AY421020 Homo sapi |
| 7 | 477.6 | 82.2 | 804 | 9 | AL157542 | AL157542 DKFZP761D |
| 8 | 477 | 82.1 | 1030 | 10 | BE793530 | BE793530 601590016 |
| 9 | 429 | 73.8 | 815 | 10 | BF785386 | BF785386 602111728 |
| 10 | 421.8 | 72.6 | 854 | 11 | AK013244 | AK013244 Mus muscu |
| 11 | 413 | 70.4 | 697 | 12 | B1770566 | B1770566 603060362 |
| 12 | 409 | 70.1 | 732 | 12 | BG298789 | BG298789 602396527 |
| 13 | 407.4 | 70.1 | 633 | 14 | CB578463 | CB578463 AMGNNUC:N |
| 14 | 403.6 | 69.5 | 560 | 10 | AM258810 | AM258810 um74a02.Y |
| 15 | 382.2 | 65.8 | 626 | 14 | CA391923 | CA391923 CS20C09.Y |
| 16 | 357.2 | 61.5 | 643 | 12 | B1910270 | B1910270 603069493 |
| 17 | 353.6 | 60.9 | 440 | 14 | CB749817 | CB749817 AMGNNUC:M |
| 18 | 348.4 | 60.0 | 559 | 13 | BY704881 | BY704881 BY704881 |
| 19 | 339 | 58.3 | 437 | 14 | CB790932 | CB790932 AMGNNUC:N |
| 20 | 335.6 | 57.8 | 358 | 14 | CF533813 | CF533813 UI-M-F10- |
| 21 | 323.8 | 55.7 | 645 | 13 | BY740551 | BY740551 BY740551 |
| 22 | 321.8 | 55.4 | 362 | 9 | AA569919 | AA569919 VO21F08.X |
| 23 | 321.8 | 55.4 | 869 | 13 | BU557268 | BU557268 AGENCOURT |
| 24 | 321.8 | 55.4 | 872 | 13 | BU557410 | BU557410 AGENCOURT |
| 25 | 317.4 | 54.6 | 548 | 14 | CA407899 | CA407899 1004048.H |
| 26 | 303.2 | 52.2 | 460 | 13 | BY285647 | BY285647 BY285647 |
| 27 | 302 | 52.0 | 410 | 14 | CB804140 | CB804140 AMGNNUC:M |
| 28 | 298 | 51.3 | 449 | 13 | BY253191 | BY253191 BY253191 |
| 29 | 283.8 | 48.8 | 1053 | 13 | BU931540 | BU931540 AGENCOURT |
| 30 | 282 | 48.5 | 758 | 12 | B1764428 | B1764428 603050701 |
| 31 | 281.4 | 48.4 | 327 | 29 | AY421021 | AY421021 Pan tLo91 |
| 32 | 272.6 | 46.9 | 457 | 10 | BB856021 | BB856021 BB856021 |
| 33 | 268.6 | 46.2 | 430 | 14 | CB760687 | CB760687 AMGNNUC:N |
| 34 | 265.2 | 45.6 | 425 | 13 | BY251598 | BY251598 BY251598 |
| 35 | 262.2 | 45.1 | 467 | 13 | BY253189 | BY253189 BY253189 |
| 36 | 261.6 | 45.0 | 302 | 13 | BY556166 | BY556166 BY556166 |
| 37 | 259 | 44.6 | 305 | 13 | BY356183 | BY356183 BY356183 |
| 38 | 249.4 | 42.9 | 749 | 12 | BG677345 | BG677345 602624059 |
| 39 | 241.6 | 41.6 | 375 | 13 | BY302913 | BY302913 BY302913 |
| 40 | 241 | 41.5 | 1064 | 13 | BQ646339 | BQ646339 AGENCOURT |
| 41 | 240 | 41.3 | 314 | 13 | BY356000 | BY356000 BY356000 |
| 42 | 239.6 | 41.2 | 353 | 13 | BY312773 | BY312773 BY312773 |
| 43 | 239.6 | 41.2 | 372 | 13 | BY133304 | BY133304 BY133304 |
| 44 | 239.4 | 41.2 | 601 | 10 | BP204905 | BP204905 601866718 |
| 45 | 238.8 | 41.1 | 452 | 14 | CB786193 | CB786193 AMGNNUC:N |

ALIGNMENTS

RESULT 1
AY421022
LOCUS
DEFINITION Mus musculus BCL2L2 gene, VIRUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY421022 GI:39776973
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
Gene titlos
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,C.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene titlos
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
 source 1..582
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>582
 /gene="Bcl2l2"
 /locus_tag="Hcm7418"

ORIGIN
 Query Match 96.4%; Score 560.2; DB 29; Length 582;
 Best local Similarity 97.8%; Pred. No. 2.8e-132;
 Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGCCGACCCGACCTTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
 Db 1 ATGGCGACCCGACCTTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
 QY 61 AGGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCGACGCGGAC 120
 Db 61 AAGCTGAGGAGAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGGCCGACGCGGAC 120
 QY 121 CCGGTGACCAAGCATGCGGGCTGTGAGAGAGAGTTTGAAGCCGTTTCGCGCGAC 180
 Db 121 CCGGTGACCAAGCATGCGGGCTGTGAGAGAGAGTTTGAAGCCGTTTCGCGCGAC 180
 QY 181 TTCTCTGACCTGGCCGCTGACGTACAGTGAACCCAGGCTGACCCGACGACGCTTAC 240
 Db 181 TTCTCTGACCTGGCCGCTGACGTACAGTGAACCCAGGCTGACCCGACGACGCTTAC 240
 QY 241 CAGGTTTCCGACGAATTTTCCAAAGGGGGCCCTTAAGTGGGGCGCTGTGGGATCTTT 300
 Db 241 CAGGTTTCCGACGAATTTTCCAAAGGGGGCCCTTAAGTGGGGCGCTGTGGGATCTTT 300
 QY 301 GTCTTTGGGGCTGCGCTGTGAGCTGAGAGTGTCAACAAAGATGAGCCCTTGTGGGA 360
 Db 301 GTCTTTGGGGCTGCGCTGTGAGCTGAGAGTGTCAACAAAGATGAGCCCTTGTGGGA 360
 QY 361 CAAATCCAGATTTGATGCTGAGCTTACCTGAGAGCAAGTGTGCTGATGATCCACAG 420
 Db 361 CAAATCCAGATTTGATGCTGAGCTTACCTGAGAGCAAGTGTGCTGATGATCCACAG 420
 QY 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTTATACGGGAGCGGGCCCTGAGAGAGCAAG 480
 Db 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTTATACGGGAGCGGGCCCTGAGAGAGCAAG 480
 QY 481 CGTCTGGGAGAGGCACTGGGCTATGATGACACATGTGTGACGGGGCCGAGGACAG 540
 Db 481 CGTCTGGGAGAGGCACTGGGCTATGATGACACATGTGTGACGGGGCCGAGGACAG 540
 QY 541 GGGGCCCTGGTAACTGTAGAGGCTTTTGTCTAGCAAGTG 581
 Db 541 GGGGCCCTGGTAACTGTAGAGGCTTTTGTCTAGCAAGTG 581

RESULT 2
 LOCUS AK015644 1949 bp mRNA linear HTC 20-SEP-2003
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493048bD08 product:Bcl2-1-like 2, full insert sequence.
 ACCESSION AK015644
 VERSION AK015644.1 GI:12854052
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1

AUTHORS
 TITLE Carninci, P. and Hayashizaki, Y.
 JOURNAL High-efficiency full-length cDNA cloning
 MEDLINE Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 9979253
 10349636

REFERENCE
 2
 TITLE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 JOURNAL Normalization and subraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20499374
 11042159

REFERENCE
 3
 TITLE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 JOURNAL RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 20530913
 11076861

REFERENCE
 4
 TITLE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 JOURNAL Functional annotation of a full-length mouse cDNA collection
 MEDLINE Nature 409, 685-690 (2001)
 PUBMED 11706861

REFERENCE
 5
 TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 JOURNAL Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 MEDLINE Nature 420, 563-573 (2002)
 PUBMED 12000000

REFERENCE
 6
 TITLE (baes 1 to 1949)
 JOURNAL Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaekawa, T., Kato, H., Kawai, D., Koizumi, Y., Kono, H., Kouda, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 JOURNAL Direct Submission
 MEDLINE Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-ree@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 PUBMED Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 11042159

COMMENT
 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCCAGAGCTCTTTTGTCTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATTCGAGTTAATTAATTAATCCGCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified plasmidscript KS(+) after bulk excision from Lambda PLO 1. Cloning sites, 5' end: SalI; 3'

end: BamHI. Host: DH10B.
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 putative"

CDS
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ORIGIN

Query Match 96.4%; Score 560.2; DB 11; Length 1949;
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 192 AAGCTGAGGACAGAGGATATGCTGTGGAGCTGGGCGCTGGAGAGCCCGCCGAC 251
 121 CGGCTGACACCAAGCCATGCGGCGCTGTGGAGACAGATTGAGACCCGCTTCCGCGCAC 180
 252 CGGCTGACACCAAGCCATGCGGCGCTGTGGAGACAGATTGAGACCCGCTTCCGCGCAC 311
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 312 TTCTCTGACCTGGCGCTCAGTACACGTCGACCCCGACCGCCAGACAGCTTACC 371
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 552 AGTGGGCGCTGGCGGACCTTCAACGCTCTATACGGGGAAGGGCCCTGGAGAGCCACAGG 611
 481 CGGCTGCGGAGGCGCACTGGGCACTGAGAGACAGTGGTACGCGGCGCTGGCACTG 540
 612 CGGCTGCGGAGGCGCACTGGGCACTGAGAGACAGTGGTACGCGGCGCTGGCACTG 671
 541 GGGGCGCTGTACTGATGAGGCGCTTTTGTGCTAGCAAGTG 581
 672 GGGGCGCTGTACTGATGAGGCGCTTTTGTGCTAGCAAGTG 712

RESULT 3

AK004680
 LOCUS
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ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
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 PUBMED
 REFERENCE
 AUTHORS

TITLE
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 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL

AK004680 3487 bp mRNA linear HTC 20-SRP-2003
 Mus musculus adult male lung cDNA, RIKEN full-length enriched
 library, clone:1200009L24 product:Bcl2-like 2, full insert
 sequence.

AK004680
 AK004680.1 GI:12836027
 HTC, CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (bases 1 to 3487)
 Aaachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furukoshi, Y.,
 Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
 Hiraoaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
 Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, K.,
 Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
 further details.

COMMENT

FEATURES

Location/Qualifiers

CDS

ORIGIN

59

569

105

SOURCE

AUTHORS

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Db 250 CCGCTGACACCAAGCCATATGCGGGCTGCTGAGACAGATTTAGAACCCGTTTCCGCCGAC 309

Qy 181 TTCTGTGACCTGGCCGCTCAAGCTACAGTACAGTGAACCCCAAGCTCAGCCAGCAAGCTTCAC 240

Db 310 TTCTGTGACCTGGCCGCTCAAGCTACAGTGAACCCCAAGCTCAGCCAGCAAGCTTCAC 369

Qy 241 CAGGTTTCCAGAGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTGTGGCACTTCT 300

Db 370 CAGGTTTCCAGAGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTGTGGCACTTCT 429

Qy 301 GTCTTTGGGGGTGCGCTTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 360

Db 430 GTCTTTGGGGGTGCGCTTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGGA 489

Qy 361 CAAGTCACGATTTGGATCTGTGGCCTTA -CTTGAAGACACGCTTGTGCTACATGATCCAC 419

Db 490 CAAGTCACGATTTGGATCTGTGGCCTTAACCTTGAAGACACGCTTGTGCTACATGATCCAC 549

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Db 550 CAGTGGGGGGCTGGGGCGAGTTCACAGCTCTTACCGGGGACGGGGCCCTTGAAGAGGCA 609

Qy 478 CGGCTCTGCGGAGAGGACCACTGGGCATAGTGAAGCAAGTGTGAC -GGGGGCGGTGGC 536

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genomic survey sequence.
AY421020
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Comment
Features
source

AY421020 582 bp DNA linear GSS 17-DEC-2003
Homo sapiens BCL2L2 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY421020.1 GI:39776977
GSS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene titros
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
Location/Qualifiers
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| DB | 361 CAAGTCCAGAGTGGATCTGGGCGCTTACCTGGAGACAGTGTGGCTGATGGATCAAGC 420 | |
| QY | 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTTACCGGAGCGGGGCTGTGATGATCAAGC 480 | |
| DB | 421 AGTGGCGGCTGGGCGGAGCTTCAAGCTCTTACCGGAGCGGGGCTGTGATGATCAAGC 480 | |
| QY | 481 CGTTCGCGGAGGCGCACTGGGCAATGATGAGACAGTGTGACGGGCGCGTGGCACTG 540 | |
| DB | 481 CGTTCGCGGAGGCGCACTGGGCAATGATGAGACAGTGTGACGGGCGCGTGGCACTG 540 | |
| QY | 541 GGGGCGCTGTGACTGTGAGGGGCGCTTTTGTCTGCAAGTG 581 | |
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| DEFINITION | DKEFp761D0816 r1 761 (synonym: hamy2) Homo sapiens cDNA clone | |
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| VERSION | AL157542.1 GI:7057943 | |
| KEYWORDS | EST. | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |
| REFERENCES | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | |
| JOURNAL | 1 (bases 1 to 804) | |
| COMMENT | Angerger, W., Winkler, U., Mewes, W., Weill, B., and Wiemann, S. | |
| | EST (Angerger, W., Winkler, U., Mewes, H.W., Weill, B. and Wiemann, S.) | |
| | Unpublished (1999) | |
| | Contact: MIPS | |
| | MIPS | |
| | Ingolstedter Landstr.1, D-85764 Neuherberg, Germany | |
| | This is the 5' sequence of the clone insert | |
| | Clone from S. Wiemann, Molecular Genome Analysis, German Cancer | |
| | Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; | |
| | sequenced by EMBL (European Molecular Biology Laboratories, | |
| | Heidelberg/Germany) within the cDNA sequencing consortium of the | |

German Genome Project.
No SI sequence available.

This clone (DKFZ761D0816) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Source 1. 804
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/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="761 (synonym: hamy2)"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN

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Best Local Similarity 91.0%; Pred. No. 4,1e-111;
Matches 529; Conservative 0; Mismatches 50; Indels 2; Gaps 2;

1 ATGCCGACCCGACGCTCAACCCGACACACGCGCTAGTGGCTGATTTGATGGCTAT 60
134 ATGCGACCCGACGCTCGGCTCCGACACACGCGCTGCTGTCGACACTTGTAGTTAT 193
61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCAGCCGCGAC 120
134 AAGCTGAGGCAAGAGGTTATGTCTGTGAGCTGGGCTGGGGAAGCCAGCAGCTGAC 253
121 CGGCTGACCAAGCCATGCGGGCTCTGGAAGAGATTGAGACCCGTTCCGCGCAC 180
254 CGGCTGACCAAGCCATGCGGGCTCTGGAAGAGATTGAGACCCGTTCCGCGCAC 313
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314 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGCTCAAGCCAGCAACGCTTAC 373
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374 CAGGTTCCGACGAATTTTCCAGAGGGGCTTACCTGAGGCGCTTGTGAGCTTCTT 433
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434 GTCTTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
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494 CAAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
421 AGTGGCGGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
554 AGTGGCGGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
481 CGTTCGCGGAGGAGCACTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
613 CGTTCGCGGAGGAGCACTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
541 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGTAAGTGTAGGGGCTTTTGTGTAAGTGT 581
672 GGGGCGCTGTAAGTGTAGGGGCTTTTGTGTAAGTGTAGGGGCTTTTGTGTAAGTGT 712

RESULT 8
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DEFINITION BE793530 Homo sapiens cdna clone IMAGE:3944307 5',
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ACCESSION BE793530
VERSION BE793530.1 GI:10214832
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 1030)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov
Plate: LLC800 row: P column: 04
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FEATURES

Source 1. 1030
Location/Qualifiers

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/note="Organ: Lung; Vector: pOT7; Site 1: XhoI; Site 2:
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 82.1%; Score 477; DB 10; Length 1030;
Best Local Similarity 88.8%; Pred. No. 6,5e-111;
Matches 516; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

1 ATGCCGACCCGACGCTCAACCCGACACACGCGCTGATGGCTGATTTGATGGCTAT 60
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384 CAGGTTCCGACGAATTTTCCAGAGGGGCTTACCTGAGGCGCTTGTGAGCTTCTT 443
301 GTCTTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
444 GTCTTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
361 CAAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
504 CAAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 563
421 AGTGGCGGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
564 AGTGGCGGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623

| | | | | |
|------------|---|-------------|--|------------------------|
| Db | | 240 | CCAAAGGAGGCCCTTAACATCGAGGC CGCTCTTGGCATTCT--TGCTTTGGAGCGTCGCTGTG | 296 |
| QY | | 321 | TGCTGAAGTGTCAACAAGAAATGAGCCTTTGTGTGGGACAAAGTCACAGATTGGATGCT | 380 |
| Db | | 297 | TGCTAAGAGTGTCAACAAGAAATGAGACC-TTGGTGGGACAAGTGCAGAGATTGGATGCT | 355 |
| QY | | 381 | GGCCTAACCTGGAGACACGCTCGGCTGACTGATCCACAGCATNGCGCGCTGGCGGACATT | 440 |
| Db | | 356 | GGCCTTAACCTGGAGACACGCTCTGGCTGACTGATCCACAGCATNGCGCGCGCTGGCGGACATT | 415 |
| QY | | 441 | CACAGCTCTATAACGGGAGACGGGGGCCCTGAGAGACGACGCGCTCTGCGGAGGCGCAACTG | 500 |
| Db | | 416 | CACAGCTCTATAACGGGAGACGGGGGCCCTGAGAGAGGACACGG-GTCTGCGGAGAGGGAMC-G | 473 |
| QY | | 501 | GGCATGAGTAGACACAGTGTGTGACCGGGGGCCCTGGCACCTGGGGGCCCTGTGTAACGTGAG | 560 |
| Db | | 474 | GGCATCAGTAGAGACAGTGTGTGACCGGGGGCCCTGGCACCT-GGGGGCCCTGTGTAACGTGAG | 532 |
| QY | | 561 | GGCGCTTTTT 569 | |
| Db | | 533 | GGCGCTTTTT 541 | |
| RESULT 10 | | | | |
| LOCUS | AK013244 | | | |
| DEFINITION | AK013244 | 854 bp | mRNA | linear HIC 20-SEP-2003 |
| | Mus musculus I0, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810435A13 product:Bcl2-l1ke 2, full insert sequence. | | | |
| ACCESSION | AK013244 | | | |
| VERSION | AK013244.1 | GI:12850487 | | |
| KEYWORDS | HIC; CAP trapper; | | | |
| SOURCE | Mus musculus (house mouse) | | | |
| ORGANISM | Mus musculus | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| REFERENCE | | | | |
| AUTHORS | Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. | | | |
| TITLE | High-efficiency full-length cDNA cloning | | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | | |
| MEDLINE | 99279253 | | | |
| PUBMED | 10349636 | | | |
| REFERENCE | | | | |
| AUTHORS | Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. | | | |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | | |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | | | |
| MEDLINE | 20499374 | | | |
| PUBMED | 11042159 | | | |
| REFERENCE | | | | |
| AUTHORS | Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tachio,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Harada,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sekiguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Iehikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. | | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer | | | |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) | | | |
| MEDLINE | 20530913 | | | |
| PUBMED | 11076861 | | | |
| REFERENCE | | | | |
| AUTHORS | The Riken Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | | | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | | |
| JOURNAL | Nature 409, 685-690 (2001) | | | |
| REFERENCE | 5 | | | |
| AUTHORS | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | | | |
| TITLE | Analysis of the mouse transcriptome based on functional annotation | | | |

JOURNAL
REFERENCE
AUTHORS
Nature 420, 563-573 (2002)
6 (bases 1 to 854)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

ORIGIN this is a NIH_MGC Library."

Query Match 71.1%; Score 413; DB 12; Length 697;
Best Local Similarity 90.1%; Pred. No. 1.2e-94;
Matches 498; Conservative 0; Mismatches 50; Indels 5; Gaps 5;

QY 1 ATGCCGACCCAGCTCAACCCCAACACACGCGCTCTAGTGGCTGATTTGAGCTAT 60
DB 145 ATGGGACCCAGCTCGGCTCCGACACACGCGCTCTAGTGGCTGATTTGAGCTAT 204
QY 61 AGGCTGAGGACAGAGGTTATCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 120
DB 205 AAGCTGAGGACAGAGGTTATCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 264
QY 121 CCGCTGACACAGGCTATGCGGGCTGCTGAGACGAGTTGAGACCTTTCCGCGCAC 180
DB 265 CCGCTGACACAGGCTATGCGGGCTGCTGAGACGAGTTGAGACCTTTCCGCGCAC 324
QY 181 TTCTGTACCTGGGCGCTCAGCTACAGTGAACCCGAGCTCAGGCCAGCAAGCTTACC 240
DB 325 TTCTGTACCTGGGCGCTCAGCTACAGTGAACCCGAGCTCAGGCCAGCAAGCTTACC 384
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAAGTGGGCTCTTGTGGCATCTTT 300
DB 385 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAAGTGGGCTCTTGTGGCATCTTT 444
QY 301 GTCTTTGGGGCTGCCCTGTG- TGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 359
DB 445 GTCTTTGGGGCTGCCCTGTG- TGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 504
QY 360 ACAAGTCCAGAGTTGAGATCGTGGCTTACT- GAGACACGCTGTGCTGATCGATCCACA 418
DB 505 ACAAGTCCAGAGTTGAGATCGTGGCTTACT- GAGACACGCTGTGCTGATCGATCCACA 564
QY 419 GCAGTGGGCGCTGGGCGGACCTTCAAGCTTATAC- GGGGACGCGGGGCGCTGGAGAGGACA 477
DB 565 GCAGTGGGCGCTGGGCGGACCTTCAAGCTTATAC- GGGGACGCGGGGCGCTGGAGAGGACA 624
QY 478 CGGCGTCTGCGGAGGCGCACTGGGCA- TGAATGACACAG- TGATGACGCGGCGCTGG 535
DB 625 CGGCGTCTGCGGAGGCGCACTGGGCACTGAGTGAACAGTTCTGACGCGGACCGCTGG 684
QY 536 CACTGGGGGCGCT 548
DB 685 CACTGGGGGCGCT 697

RESULT 12
LOCUS BG298789 792 bp mRNA linear EST 21-FEB-2001
DEFINITION 602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:451125 5',
RNA sequence.
ACCESSION BG298789
VERSION BG298789.1 GI:13063794
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

FEATURES
Source Plate: LLAM10394 row: e column: 08
High quality sequence stop: 713.
Location/Qualifiers
1..792

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:451125"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-Sport6; Site: 1; No: 1;
Site: 2; Salt: Cloned unidirectionally; oligo-dt primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.4%; Score 409; DB 12; Length 792;
Best Local Similarity 97.5%; Pred. No. 1.4e-93;
Matches 426; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ATGCCGACCCAGCTCAACCCCAACACACGCGCTCTAGTGGCTGATTTGAGCTAT 60
DB 99 ATGGGACCCAGCTCGGCTCCGACACACGCGCTCTAGTGGCTGATTTGAGCTAT 158
QY 61 AGGCTGAGGACAGAGGTTATCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 120
DB 159 AAGCTGAGGACAGAGGTTATCTGTGAGCTGGGCTGGGAGAGGCCGACCCGAC 218
QY 121 CCGCTGACACAGGCTATGCGGGCTGCTGAGACGAGTTGAGACCTTTCCGCGCAC 180
DB 219 CCGCTGACACAGGCTATGCGGGCTGCTGAGACGAGTTGAGACCTTTCCGCGCAC 278
QY 181 TTCTGTACCTGGGCGCTCAGCTACAGTGAACCCGAGCTCAGGCCAGCAAGCTTACC 240
DB 279 TTCTGTACCTGGGCGCTCAGCTACAGTGAACCCGAGCTCAGGCCAGCAAGCTTACC 337
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAAGTGGGCTCTTGTGGCATCTTT 300
DB 338 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAAGTGGGCTCTTGTGGCATCTTT 397
QY 301 GTCTTTGGGGCTGCCCTGTG- TGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 360
DB 398 GTCTTTGGGGCTGCCCTGTG- TGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGG 457
QY 361 CAAGTCCAGAGTTGAGATCGTGGCTTACCCTGAGACACGCTGGGCTGATCGATCCACAGC 420
DB 458 CAAGTCCAGAGTTGAGATCGTGGCTTACCCTGAGACACGCTGGGCTGATCGATCCACAGC 517
QY 421 AGTGGCGCTGGGCGGA 437
DB 518 AGTGGCGCTGGGCGGA 534

RESULT 13
LOCUS CB578463 623 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:NR001-00100-H10-A nr001 (10855) Rattus norvegicus cDNA
clone nr001-00100-h10 5', mRNA sequence.
ACCESSION CB578463
VERSION CB578463.1 GI:29522504
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 623)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick

Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00100 row: h column: 10.

FEATURES

source

1..623
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdd1-00100-110"
/issue_type="Dorsal Root Ganglia"
/clone_lib="nrdd1 (10855)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat dorsal root ganglia"

ORIGIN

Query Match 70.1%; Score 407.4; DB 14; Length 623;
Best Local Similarity 96.3%; Pred. No. 3.2e-93;
Matches 417; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCAGGCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 191 ATGGCGACCCAGGCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 250
QY 61 AGGCTGAGGAGGAGGAGGTTATGTCTGTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 251 AAGCTGAGGAGGAGGAGGTTATGTCTGTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 310
QY 121 CCGCTGACCAAGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTTCCGCGCGAC 180
DB 311 CCGCTGACCAAGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTTCCGCGCGAC 370
QY 181 TTCTGTACCTGGCGGCTCAAGTCAAGTCAAGCCAGGCTCAAGCCAGCAAGCTTCAC 240
DB 371 TTCTGTACCTGGCGGCTCAAGTCAAGTCAAGCCAGGCTCAAGCCAGCAAGCTTCAC 430
QY 241 CAGGTTCCGACGAACTTTCCAAAGGGGGCCCTAAGTGGGGCCGCTCTGAGGACTTT 300
DB 431 CAGGTTCCGACGAACTTTCCAAAGGGGGCCCTAAGTGGGGCCGCTCTGAGGACTTT 490
QY 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 360
DB 491 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCATTTGTGGGA 550
QY 361 CAAGTCAGAGATTGATGCTGTGGCTTACCTGGAAGACAGCTGTGGCTGACTGATCCACAG 420
DB 551 CAAGTCAGAGATTGATGCTGTGGCTTACCTGGAAGACAGCTGTGGCTGACTGATCCACAG 610
QY 421 AGTGGCGGCTGGG 433
DB 611 AGTGGCGGCTGGG 623

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RESULT 14
AM258810 540 bp mRNA linear EST 23-DEC-1999
LOCUS AM258810
DEFINITION IMAG2:2300906 5' similar to SW:BCIW MOUSE P70345 APOPTOSIS
ACCESSION AM258810
VERSION AM258810.1 GI:6631791
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 540)
AUTHORS Martini, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL

Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

COMMENT

Email: mouseest@wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:1009678
Seq primer: custom primer used
High quality sequence stop: 465.

FEATURES

source

1..540
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL"
/db_xref="taxon:10090"
/clone="IMAG2:2300906"
/sex="female"
/dev_stage="adult"
/lab_host="DHI0B"

ORIGIN

Query Match 69.5%; Score 403.6; DB 10; Length 540;
Best Local Similarity 97.7%; Pred. No. 2.8e-92;
Matches 420; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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QY 1 ATGCCGACCCAGGCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB 112 ATGGGACCCAGGCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 171
QY 61 AGGCTGAGGAGGAGGTTATGTCTGTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
DB 172 AAGCTGAGGAGGAGGTTATGTCTGTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 231
QY 121 CCGCTGACCAAGCCATGCGGCTGTGTGAGAGAGAGATTGAGACCCGTTTCCGCGAC 180
DB 232 CCGCTGACCAAGCCATGCGGCTGTGTGAGAGAGAGATTGAGACCCGTTTCCGCGAC 291
QY 181 TTCTGTACCTGGCGGCTCAAGTCAAGTCAAGCCAGGCTCAAGCCAGCAAGCTTCAC 240
DB 292 TTCTGTACCTGGCGGCTCAAGTCAAGTCAAGCCAGGCTCAAGCCAGCAAGCTTCAC 351
QY 241 CAGGTTTCCGACGAACTTTCCAAAGGGGGCCCTAAGTGGGGCCGCTGTGGACTTT 300
DB 352 CAGGTTTCCGACGAACTTTCCAAAGGGGGCCCTAAGTGGGGCCGCTGTGGACTTT 411
QY 301 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 360
DB 412 GTCTTTGGGGCTGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 471
QY 361 CAAGTCAGAGATTGATGCTGTGGCTTACCTGGAAGACAGCTGTGGCTGACTGATCCACAG 420
DB 472 CAAGTCAGAGATTGATGATGCTGTGGCTTACCTGGAAGACAGCTGTGGCTGACTGAT- CACAGC 530
QY 421 AGTGGCGGCT 430
DB 531 AGTGGCGGCT 540

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RESULT 15

CA391923

LOCUS

CA391923

626 bp mRNA linear EST 06-NOV-2002
ca20c09.y1 Human Retinal pigment epithelium/choroid cDNA
(un-normalized, unamplified): cs Homo sapiens cDNA clone ca20c09

5', mRNA sequence.

ACCESSION

CA391923

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 626)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Parrie,R.N., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPE/choroid for the
NEI/NIH Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gwaeme@helix.nih.gov
Plate: 20 row: C column: 09
Seg primer: M13RPI reverse primer (ABI).

FEATURES

Source

1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ca20c09"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMD10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: PCWVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pcwvSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>". The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 65.8%; Score 382.2; DB 14; Length 626;

Best Local Similarity 90.3%; Pred. No. 8.8e-877

Matches 408; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60

175 ATGGCGACCCAGCCTCGGCCCGACACACGCGCTCTGCTGCGACACTTTGAGTTAT 224

61 AGGCTGAGGAGAAAGGTTATCTGTGAGCTGCGCTGCGGAAAGGCCAGCCGCGAC 120

235 AAGCTGAGGAGAAAGGTTATCTGTGAGCTGCGGCCCGGAGGCGCGACGCTGAC 294

121 CCGCTGCACCAAGCATGCGGCTGCTGAGACGAGATTGAGACCCGTTTCGCGCGACC 180

295 CCGCTGCACCAAGCATGCGGCTGCTGAGACGAGATTGAGACCCCGTTCCGCGCAC 354

181 TTCTGTGACCTGAGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAAGCTTAC 240

355 TTCTGTGATCTGCGCGCTCAGCTGATGTGACCCAGGCTCAGCCAGCAAGCTTAC 414

241 CAGGTTTCGACGAACCTTTCCAGGCGGCCCTTAAGTGGGCGCTTTGGCAATCTTT 300

415 CAGGTCCTCGAATGAACCTTTTCAAGGCGGCCCAACTGGGCGCCCTTGTAGCCCTTT 474

301 GTCTTTGGGCGCTGCCCTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTTGGG 360

475 GTCTTTGGGCGCTGCACTGTGTGCTGAGAGTGTCAAAAGAAATGAGCCCTTTGG 534

361 CAAATCCAGGATTTGATGCTGAGCTTACCTGAGACACGCTGCTGACTGATCCACG 420

535 CAAATCCAGGATTTGATGCTGAGCTTACCTGAGACACGCTGCTGACTGATCCACG 594

421 AGTGGCGGCTGGCGCGAAGTTCAAGCTCTATA 452

595 AGTGGCGGCTGGCGCGAAGTTCAAGCTCTATA 626

Search completed: March 29, 2004, 07:28:10
Job time : 2269.1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:01:08 / Search time 2753.26 Seconds

(without alignments)
9146.355 Million cell updates/sec

Title: US-09-155-327G-8

Perfect score: 581

Sequence: 1 atgcgcaccacagctcaac.....gcttttttgcagcaagtg 581

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_srs:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pin:*
35: em_hg_rtd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sv:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|-----------------------|
| 1 | 581 | 100.0 | 581 | 6 | AX022531 | AX022531 Sequence |
| 2 | 581 | 100.0 | 581 | 6 | AX030819 | AX030819 Sequence |
| 3 | 560.2 | 96.4 | 582 | 10 | MMT59746 | U59746 Mus musculus |
| 4 | 560.2 | 96.4 | 3476 | 10 | AF030769 | AF030769 Mus musculus |
| 5 | 544.2 | 93.7 | 582 | 10 | AF096291 | AF096291 Rattus no |
| 6 | 544.2 | 93.7 | 1110 | 10 | AY185100 | AY185100 Rattus no |
| 7 | 544.2 | 93.7 | 3487 | 10 | AY185098 | AY185098 Rattus no |
| 8 | 541 | 93.1 | 3473 | 10 | AY170344 | AY170344 Mus musculus |
| 9 | 540.6 | 93.0 | 579 | 6 | AR020779 | AR020779 Sequence |
| 10 | 505.8 | 87.1 | 582 | 6 | AX461423 | AX461423 Sequence |
| 11 | 505.8 | 87.1 | 582 | 9 | HSU59747 | U59747 Human Bcl-2 |
| 12 | 502.6 | 86.5 | 3542 | 9 | D87461 | D87461 Human mRNA |
| 13 | 501 | 86.2 | 583 | 6 | AX022529 | AX022529 Sequence |
| 14 | 501 | 86.2 | 583 | 6 | AX030817 | AX030817 Sequence |
| 15 | 457.4 | 85.6 | 579 | 6 | AR020780 | AR020780 Sequence |
| 16 | 451.4 | 77.7 | 220818 | 2 | AC128940 | AC128940 Rattus no |
| 17 | 451.4 | 77.7 | 223933 | 2 | AC097389 | AC097389 Rattus no |
| 18 | 421.8 | 72.6 | 3815 | 10 | BC040369 | BC040369 Mus musculus |
| 19 | 421.8 | 72.6 | 237561 | 10 | AC116591 | AC116591 Mus musculus |
| 20 | 407.4 | 70.1 | 210784 | 2 | AC119293 | AC119293 Rattus no |
| 21 | 407.4 | 70.1 | 263901 | 2 | AC115371 | AC115371 Rattus no |
| 22 | 390.8 | 67.3 | 148278 | 2 | AC079885 | AC079885 Rattus no |
| 23 | 390.8 | 67.3 | 180655 | 2 | AC084240 | AC084240 Rattus no |
| 24 | 390.8 | 67.3 | 221557 | 2 | AC134055 | AC134055 Rattus no |
| 25 | 364.8 | 62.8 | 1098 | 6 | AR432565 | AR432565 Sequence |
| 26 | 364.8 | 62.8 | 1098 | 6 | BD078624 | BD078624 Human pro |
| 27 | 364.4 | 62.7 | 1864 | 6 | BD191165 | BD191165 186 human |
| 28 | 364.2 | 62.7 | 196292 | 9 | CNS0000B | AL049829 Human chr |
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| 31 | 212.2 | 36.5 | 6049 | 6 | AX345130 | AX345130 Sequence |
| 32 | 191 | 32.9 | 6049 | 6 | AX345131 | AX345131 Sequence |
| 33 | 142.4 | 24.5 | 1252 | 4 | AB073983 | AB073983 Canis fam |
| 34 | 140.8 | 24.2 | 1163 | 4 | AB080951 | AB080951 Felis cat |
| 35 | 139.2 | 23.8 | 702 | 4 | AY005131 | AY005131 Oryctolag |
| 36 | 138.2 | 23.8 | 1184 | 5 | GGU26645 | U26645 Gallus gall |
| 37 | 137.6 | 23.7 | 541 | 4 | AF245488 | AF245488 Bos tauru |
| 38 | 137.6 | 23.7 | 766 | 4 | AF164517 | AF164517 Ovis arie |
| 39 | 136 | 23.4 | 541 | 4 | AF245487 | AF245487 Bos tauru |
| 40 | 136 | 23.4 | 541 | 4 | AF245489 | AF245489 Bos tauru |
| 41 | 134.6 | 23.2 | 636 | 6 | BD097037 | BD097037 A. BH4 fus |
| 42 | 134.6 | 23.2 | 702 | 6 | BD084108 | BD084108 Method of |
| 43 | 134.6 | 23.2 | 702 | 6 | BD102202 | BD102202 Method of |
| 44 | 134.6 | 23.2 | 702 | 9 | BT007208 | BT007208 Homo sapi |
| 45 | 134.6 | 23.2 | 702 | 12 | BT008248 | BT008248 Synthetic |

ALIGNMENTS

RESULT 1
AX022531
LOCUS AX022531 581 bp DNA
DEFINITION Sequence 8 from Patent EP0932674.
ACCESSION AX022531
VERSION AX022531.1 GI:10046127
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Adams, J. M., Holmgren, S. P., Cory, S. and Gibson, L. M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 8 04-AUG-1999;

FEATURES

source

CDS

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ORIGIN

Query Match 100.0%; Score 581; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 6.5e-126;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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361 CAAATCCAGATTTGATGCTGCTTAACTGGAGACAGCTGTGCTGATGATCCACAG 420
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481 CGTCTGGGAGAGGCACTGGGCACTGAGTGAAGCACTGAGTGAAGGAGGCGGCTGG 540
481 CGTCTGGGAGAGGCACTGGGCACTGAGTGAAGCACTGAGTGAAGGAGGCGGCTGG 540
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541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 2
AX030819 581 bp DNA linear PAT 20-SEP-2000
LOCUS
DEFINITION Sequence 8 from Patent WO9735971.
ACCESSION AX030819
VERSION AX030819.1 GI:10278313
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE

1
Adams, J.M., Holmgren, S.P., Cory, S., and Gibson, L.M.
A novel mammalian gene, bcl-2, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-OCT-1997
ADAMS JERRY MCKEE (AU) ; HOLMGREN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEBONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

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RLREGNWA"

ORIGIN

Query Match 100.0%; Score 581; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 6.5e-126;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCCACCCACCCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
1 ATGCCACCCACCCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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61 AGGCTAGGACAGAGGGTTATGCTGTGAGCTGGGCTGGGAAAGGCCACCCCGAC 120
121 CCAGTCACCAACGCAATGCGGGCTGTGAGACGAGTTTGAACCCGTTCCGCGCAC 180
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541 GGGGCGCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581
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RESULT 3
MM059746 582 bp mRNA linear ROD 29-SEP-1996
LOCUS
DEFINITION Mus musculus Bcl-2 (bcl-2) mRNA, complete cds.

```

ACCESSION   US9746
VERSION     US9746.1
KEYWORDS    GI:1572494
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 582)
AUTHORS     Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
            Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M., and Cory, S.
            bcl-2, a novel member of the bcl-2 family, promotes cell survival
            Oncogene 13 (4), 665-675 (1996)
JOURNAL     96358615
MEDLINE     8761287
PUBMED      2 (bases 1 to 582)
REFERENCE   Gibson, L., Holmgren, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
            Cory, S.
            Direct Submission
            Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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Query Match      96.4%; Score 560.2; DB 10; Length 582;
Best Local Similarity 97.8%; Pred. No. 5e-121;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATCCGACCCAGCCTCAACCCGACACACACGCGCTCTGTGTGCTGACTTTGTAGGCTAT 60
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DB 61 AAGCTGAGGAGAGAGGCTTATGTCTGTGAGAGCTGGGCTGGGGAAGGCCACGCCGCGAC 120
QY 121 CCGCTGACCAACCCAGCCTCAACCCGACACACGCGCTCTGTGTGCTGACTTTGTAGGCTAT 180
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DB 301 GTCTTTGGGGGCTGCTGTGTGTGTGAGAGTCAACAAAGAAATGAGAGCTTTGGTGGGA 360
QY 361 CAGTCAGAGATTGATTCGTGGCTTACCTGAGACACGCTCTGGCTACTGATCCACAGC 420
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DB 421 AGTGCGGCTGGGCGGCGGACTTCAACAGCTCTTATACGGGACCGGGCCCTTGAGACGACG 480
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DB 481 CGTCTGCGGAGAGGCAACTGGGCAATGATGAGACAGTGTGAACGGGGCCCTGGGCACTG 540
QY 541 GGGGCGCTGTGTAAGTGAAGGCGCTTTTGTGTAAGCAAGTG 581
DB 541 GGGGCGCTGTGTAAGTGAAGGCGCTTTTGTGTAAGCAAGTG 581

RESULT 4
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LOCUS     Mus musculus BCL-W (Bcl-2) mRNA, complete cds.
DEFINITION
ACCESSION AF030769
KEYWORDS  AF030769.1 GI:2623249
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3476)
AUTHORS   Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and
            MacGregor, G.R.
            Bcl-2 is required for testis homeostasis
            Unpublished
            2 (bases 1 to 3476)
            Ross, A.J. and MacGregor, G.R.
            Direct Submission
            Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
            University, 1462 Clifton Road, Atlanta, GA 30322, USA
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Query Match 96.4%; Score 560.2; DB 10; Length 3476;
 Best Local Similarity 97.8%; Pred. No. 3,8e-121;
 Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGCCGACCCCAAGGCTCTCAACCCCAACACAGCGCTCTAGTGTGACTTTGAGCTAT 60
 DB 179 ATGGGAGACCCCAAGGCTCTCAACCCCAACACAGCGCTCTAGTGTGACTTTGAGCTAT 228
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 DB 239 AAGCTGAGGCAAGGCTTATGTGTGAGCTGTGGGCTGTGGGAGGCGCCAGCCGCGAC 298
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 DB 239 CCGCTGACCAAGCCATCGGGCTGTGGAGACAGATTGAGACCCGCTTCCGCGGACC 358
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 QY 241 CAGGTTTCCGACCAAGCTTTCCAGAGGGGGCCCTTAAGTGGGCGCTTGTGGATCTTT 300
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 DB 659 CGTCTGCGGAGGAGCACTGGGCACTGAGTGAAGCAGTGTGAGCGGGCCCTTGAGACTG 718
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 DB 719 GGGGCTCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 759

RESULT 5
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 LOCUS Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.

DEFINITION AF096291
 ACCESSION AF096291.1 GI:3747129
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Rattus norvegicus (Norway rat)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 582)
 Hammer, S., Skogjose, Y. and Lindholm, D.
 Differential expression of bcl-w and bcl-x messenger RNA in the
 developing and adult rat nervous system

JOURNAL Neuroscience 91 (2), 673-684 (1999)
 MEDLINE 99292146
 PUBMED 10366024

REFERENCE 2 (bases 1 to 582)
 Hammer, S., Skogjose, Y. and Lindholm, D.
 Direct Submission
 Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
 University, Box 587, BMC, Uppsala 751 23, Sweden

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ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 582;
 Best Local Similarity 96.0%; Pred. No. 2.9e-117;
 Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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 QY 481 CGTCTGCGGAGGAGCACTGGGCACTGAGTGAAGCAGTGTGAGCGGGCCCTTGAGACTG 540
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 DB 541 GGGGCTCTGTAACTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 6
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 LOCUS Rattus norvegicus BCL-WB1 mRNA, complete cds.
 DEFINITION AY185100
 ACCESSION AY185100.1 GI:32185284
 VERSION
 KEYWORDS

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)

JOURNAL MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 1110)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers

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CDS
ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 1110;
Best Local Similarity 96.0%; Pred. No. 2.6e-117;
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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301 GTCTTTGGGGGCTGCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGAGCTTTGGTGG 360
809 GTCTTTGGGGGCTGCTGTGTGTGTGAGAGTGTCAACAAAGAAATGAGAGCTTTGGTGG 868
361 CAAAGTCAGAGATTTGATCGTGGCTTACCTGAGAGACACGCTGAGTGAATTCACAGC 420
869 CAAAGTCAGAGATTTGATCGTGGCTTACCTGAGAGACACGCTTGTGATTCACAGC 928
421 AGTGGGAGCTGGGCGGACTTCAAGTCTTATAAGGGGAGCGGGCCCTGGAGGACGACG 480
929 AGTGGGAGCTGGGCGGAGTTCAAGTCTTATAAGGGGAGCGGGCCCTGGAGGAGGACG 988
481 CGTTCGCGGAGGAGCACTTGAGCATGATGAGACACAGTGTGACGAGGGGCGCTGGCACTG 540

Db 969 CGTCTGGGGAGGGAACTGGGCATCAGTAGAGCACTGCTGACGGGGCTGTGGCACTG 1048

Qy 541 GGGGCGCTGTGACTGTAGGGGCTTTTGTCTGACAGTG 581

Db 1049 GGGGCGCTGTGACTGTAGGGGCTTTTGTCTGACAGTG 1089

RESULT 7
LOCUS AY185098 3487 bp mRNA linear ROD 24-JUN-2003
DEFINITION Rattus norvegicus BCL-W mRNA, complete cds.
ACCESSION AY185098
VERSION AY185098.1 GI:32185280
KEYWORDS

SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)

JOURNAL MEDLINE 22672518
PUBMED 12787069

REFERENCE 2 (bases 1 to 3487)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center
Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers

FEATURES
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CDS
ORIGIN

Query Match 93.7%; Score 544.2; DB 10; Length 3487;
Best Local Similarity 96.0%; Pred. No. 2.1e-117;
Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

1 ATGCCGACCCCAAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGTAGCTAT 60
170 ATGCCGACCCCAAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGTAGCTAT 229
61 AGGCTGAGCGAAGAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGCCCAAGCCCGAC 120
230 AGGCTGAGCGAAGAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGCCCAAGCCCGAC 289
121 CCGCTGACCAAGCACTGGGGGCTGTGAGAGAGATTGAGACCCGTTCCGCGGCACC 180
290 CCGCTGACCAAGCACTGGGGGCTGTGAGAGAGATTGAGACCCGTTCCGCGGCACC 349
181 TTCTGTGACCTGGGCTGAGTACAGTACACCCAGCTCAGCCAGCAAGCTTACAC 240
350 TTCTGTGACCTGGGCTGAGTACAGTACACCCAGCTCAGCCAGCAAGCTTACAC 409
241 CAGGTTTCGACGAATTTTCAAGGGGCGCTTAACCTGGGGCGCTTGTGTGCAATCTT 300
410 CAGGTTTCGACGAATTTTCAAGGGGCGCTTAACCTGGGGCGCTTGTGTGCAATCTT 469

| | | | | |
|---------------------------|--|--|--|-----------------------------|
| QY | | 301 | GTCTTTGGGAGTGCCCGTGTGGCTGAGAGTGTCACAAAGAAATGAGAGCCTTTGGTGGGA | 360 |
| Db | | 470 | GTCITTTGGGAGTGCCCGTGTGTGTGTAAGAAGTGCACAACAAAGAAATGAGAGCATTGTGTGGGA | 529 |
| QY | | 361 | CAAGTCAGAGATTGGATCGTGTGGCCTTACTCGTAGAGACAGCTGTGCTGTGACTGGATCCAGAGC | 420 |
| Db | | 530 | CAGATGACGAGATTGGATGTGTGATCCTTACTCGTAGAGACAGCCTTGTGCTGTGACTGGATCCAGAGC | 589 |
| QY | | 421 | AGTGGCGGCTTGGGCGGACATTTCACAGCTCTATACGGGGAACGGGAGCCTCGAAGACGACAGC | 480 |
| Db | | 590 | AGTGGGAGGCTTGGGCGGAGGTTTACAGAGCTTATACGGGGAACGGGAGCCTCGAAGAGGACAGC | 649 |
| QY | | 481 | CGTCTGCGGAGGCGCACTGGGCGCATGAGTGACCAAGTGTGATACGCGGAGGCCGTGTGGCACTG | 540 |
| Db | | 650 | CGTCTGCGGAGGCGGAACTGGGCGCATCAAGTGAGGACAGAGTGTGACGCGGAGGCGCTGTGTGGCACTG | 709 |
| QY | | 541 | GGGGCCCTTCGTAACCTGTAAGGGGCGCTTTTTTGTGCTAGCAAGTG | 581 |
| Db | | 710 | GGGGCCCTTCGTAACCTGTAAGGGGCGCTTTTTTGTGCTAGCAAGTG | 750 |
| RESULT 8 | | | | |
| AY170344 | | | | |
| LOCUS | | AY170344 | 3473 bp | mRNA linear ROD 22-SEP-2003 |
| DEFINITION | | Mus musculus Bcl12-like protein 2 mRNA, complete cds. | | |
| ACCESSION | | AY170344 | | |
| VERSION | | AY170344.2 | GI:34857712 | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | | Mus musculus (house mouse) | | |
| | | Mus musculus | | |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| REFERENCE | | 1 (bases 1 to 3473) | | |
| AUTHORS | | Su,H.-Y. | | |
| TITLE | | Extraction from neonatal mouse skin after IGF-1 stimulation | | |
| JOURNAL | | Unpublished | | |
| REFERENCE | | 2 (bases 1 to 3473) | | |
| AUTHORS | | Su,H.-Y. | | |
| TITLE | | Direct Submision | | |
| JOURNAL | | Submitted (29-Oct-2002) Biotechnology, Pingtung University, No. 1, | | |
| | | Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan | | |
| | | (bases 1 to 3473) | | |
| REFERENCE | | 3 | | |
| AUTHORS | | Su,H.-Y. | | |
| TITLE | | Direct Submision | | |
| JOURNAL | | Submitted (22-SEP-2003) Biotechnology, Pingtung University, No. 1, | | |
| | | Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan | | |
| | | Sequence update by submitter | | |
| | | On Sep 22, 2003 this sequence version replaced gi:27497698. | | |
| REMARK | | | | |
| COMMENT | | | | |
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| | | /tissue_type="skin" | | |
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| | | GAALCAASVYKMEPLVYGVDPMWVAIETFLATWIHSSGMAEFTALLYGDGLAEARR | | |
| | | FLREGNNAASVTYLTGAVALCALTYVGAFAFYAK" | | |
| CDS | | | | |
| ORIGIN | | | | |
| Query Match | | 93.1% | Score 541; | DB 10; Length 3473; |
| Blast Local Similarity | | 95.7%; | Pred. N0.12e-116; | |
| Matches 556; Conservative | | 0; | Mismatches 25; | Indels 0; Gaps 0; |

| QY | ATGCCAGCCCGAGCTCAACCCCGACACACGCGCTTAAGTGGCTGACTTTGTAGCTAT | 60 |
|------------|--|-----------------------------------|
| Db | 182 ATGCCAGCCCGAGCTCAACCCCGACACACGCGCTTAAGTGGCTGACTTTGTAGCTAT | 241 |
| QY | 61 AGCTGAGGAGAGAGGTTATATGCTGTGAGACTGGGCTGGGAGAGGCCAGCCGCGAC | 120 |
| Db | 242 CAGCTGAGGAGAGAGGTTATATGCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCCGCGAC | 301 |
| QY | 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAACCCGTTTCCGCGAC | 180 |
| Db | 302 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAACCCGTTTCCGCGAC | 361 |
| QY | 181 TTCTCTGACTGGCGGCTCAGCTTCAAGTGAACCCCAAGCTCAAGCCAGCAAGCTTCAAC | 240 |
| Db | 362 TTCTCTCAGCTGGCGGCTCAGCTTCAAGTGAACCCCAAGCTCAAGCCAGCAAGCTTCAAC | 421 |
| QY | 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGAGCCCTTACCTGAGGAGCCGCTTGTGGACTTT | 300 |
| Db | 422 CAGGTTTCCGACGAACCTTTTCCAAAGGGGAGCCCCCACTGGGAGCCGCTTGTGGACTTT | 481 |
| QY | 301 GTCTTTGGGAGCTGGCCCTGTGTGCTGAGAGTGTCAACAAAGATGAGACCTTTGGTGGGA | 360 |
| Db | 482 GTCTTTGGGAGCTGGCCCTGTGTGCTGAGAGAGTGTCAACAAAGATGAGACCTTTGGTGGGA | 541 |
| QY | 361 CAACTGCAGATTGATGCTGAGCTTACCTGAGACACAGCTGCTGACTGAGTCCACAGC | 420 |
| Db | 542 CAACTGCAGATTGATGAGTGTGAGCTTACCTGAGACACAGCTGCTGACTGAGTCCACAGC | 601 |
| QY | 421 AGTGGCGGCTGGGCGGACTTCAACAGCTCTATACGGGGACCGGGGCGCTGGAGAGACGACCG | 480 |
| Db | 602 AGTGGCGGCTGGGCGGAGTTTCAACAGCTCTATACGGGGACCGGGGCGCTGGAGAGAGCGACCG | 661 |
| QY | 481 CGTCTGGGGAGGGGCAACTGGGGCATGTAGTGAAGACAGTGGTGAACGGGGGCGCTGGAGACTG | 540 |
| Db | 662 CGTCTGGGGAGGGGCAACTGGGGCATGTAGTGAAGACAGTGGTGAACGGGGGCGCTGGAGACTG | 721 |
| QY | 541 GGGGCGCTGTGTAAGTGAAGGGGCGCTTTTGTGCTAGCAAGTG | 581 |
| Db | 722 GGGGCGCTGTGTAAGTGAAGGGGCGCTTTTGTGCTAGCAAGTG | 782 |
| RESULT 9 | | |
| LOCUS | AR020779 | 579 bp DNA linear PAT 05-DEC-1998 |
| DEFINITION | Sequence 1 from patent US 5789201. | |
| ACCESSION | AR020779 | |
| VERSION | AR020779.1 | GI:3975394 |
| KEYWORDS | | |
| SOURCE | Unknown. | |
| ORGANISM | Unknown. | |
| REFERENCE | Unclassified. | |
| AUTHORS | 1 (bases 1 to 579) | |
| TITLE | Guestella J. | |
| JOURNAL | Genes coding for bcl-y a bcl-2 homologue | |
| FEATURES | Patent: US 5789201-A 1 04-AUG-1998; | |
| | Location/Qualifiers | |
| | 1..579 | |
| | /organism="Unknown" | |
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| ORIGIN | | |
| | Query Match 93.0%; Score 540.6; DB 6; Length 579; | |
| | Best Local Similarity 95.9%; Pred. No. 2e-116; | |
| | Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0; | |
| QY | 1 ATGCCAGCCCGAGCTCAACCCCGACACACGCGCTTAAGTGGCTGACTTTGTAGCTAT | 60 |
| Db | 1 ATGCCAGCCCGAGCTCAACCCCGACACACGCGCTTAAGTGGCTGACTTTGTAGCTAT | 60 |
| QY | 61 AGGCTGAGGAGAGAGGTTATGCTGTGAGACTGGGCTGGGAGAGGCCAGCCGCGAC | 120 |
| Db | 61 AAGCTGAGAGAGAGGTTATGCTGTGAGAGCTGGCCCTGGGAGAGGCCAGCCGCGAC | 120 |

QY 121 CCGCTGCAACCAAGCATGCGGCTGTGAGAGAGATTGAGACCCGTTTCGCGCACC 180
DB 121 CCGCTGCAACCAAGCATGCGGCTGTGAGAGAGATTGAGACCCGTTTCGCGCACC 180
QY 181 TTCTGTGACTGCGGCTGCTGAGTACAGTACCCAGGCTGACCCAGCAACGCTTACC 240
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QY 241 CAGGTTTCCGAGCACTTTTCAAGGGGGCCCTAATGAGGCGCTTGTGGCAATCTTT 300
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QY 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
QY 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGACACGCTGCTGATGATCCACAGC 420
DB 361 CAAGTCCAGAGATTGATGAGTGTGACCTACCTGAGACACGCTTGTGATCCACAGC 420
QY 421 AGTGGCGGCTGGGCGGACCTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480
DB 421 AGTGGCGGCTGGGCGGACCTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480
QY 481 CGTCTGCGGGAGGGGACCTGCGGACATGAGAGACAGTGTGACGGGGGCTGTGGCACTG 540
DB 481 CGTCTGCGGGAGGGGACCTGCGGACATGAGAGACAGTGTGACGGGGGCTGTGGCACTG 540
QY 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGCTAGCAAG 579

RESULT 10
AX481423 582 bp DNA linear PAT 16-AUG-2002
LOCUS AX481423
DEFINITION Sequence 37 from Patent WO02055693.
ACCESSION AX481423.1 GI:22316337
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Kreutzer, R., Limer, S., Roat, S. and Hadwiger, P.
JOURNAL Method for inhibiting the expression of a target gene
AUTHORS Patent: WO 02055693-A 37 18-JUL-2002,
Ridopharma AG (DE)
FEATURES
source 1..582
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 3e-108;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 181 TTCTGTGACTGCGGCTGCTGAGTACAGTACCCAGGCTGACCCAGCAACGCTTACC 240
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DB 241 CAGGTTTCCGAGCACTTTTCAAGGGGGCCCTAATGAGGCGCTTGTGGCAATCTTT 300
QY 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
DB 301 GTCTTTGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCTTTGGTGGGA 360
QY 361 CAAGTCCAGAGATTGATGCTGAGCTTACCTGAGACACGCTGCTGATGATCCACAGC 420
DB 361 CAAGTCCAGAGATTGATGAGTGTGACCTACCTGAGACACGCTGCTGATGATCCACAGC 420
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DB 421 AGTGGCGGCTGGGCGGACCTTACAGCTCTATACGGGGACGGGGCCCTGAGAGACGACGG 480
QY 481 CGTCTGCGGGAGGGGACCTGCGGACATGAGAGACAGTGTGACGGGGGCTGTGGCACTG 540
DB 481 CGTCTGCGGGAGGGGACCTGCGGACATGAGAGACAGTGTGACGGGGGCTGTGGCACTG 540
QY 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGCTAGCAAG 581
DB 541 GGGGCGCTGTGACTGAGGGGCTTTTGTGCTAGCAAG 581

RESULT 11
HSU59747 582 bp mRNA linear PRI 29-SEP-1996
LOCUS HSU59747
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION U59747
VERSION U59747.1 GI:1572492
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 582)
MEDLINE 96358615
PUBMED 8761287
REFERENCE 2 (bases 1 to 582)
AUTHORS Gibson, L., Holmgren, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.
TITLE Bcl-w, a novel member of the bcl-2 family, promotes cell survival
JOURNAL Oncogene 13 (4), 665-675 (1996)
AUTHORS
FEATURES
source 1..582
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TRANSLATION="MTPASAPDTALVADPYGYLRLRKGYICAGPBGPAADPLHQ
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GALCAESVNEKMEPLVQGVQVEMVAVYETRLADWIHSSGWAETALYGGALAEAR

AX022529
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent EP0932674.
ACCESSION AX022529
VERSION AX022529.1 GI:10046125
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
FEATURES
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RLREGNMAVSRVTLTGAVLALVTGAFPAFK"
ORIGIN
Query Match 86.2%; Score 501; DB 6; Length 583;
Best Local Similarity 91.4%; Pred. No. 4e-107;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCAAGCTTCAACCCGACACACGCGCTTATGTGGCTGACTTTGTAGCTAT 60
DB 1 ATGGCGACCCCAAGCTTCAACCCGACACACGCGCTTATGTGGCTGACTTTGTAGCTAT 60
QY 1 AGGCTGAGGCGAAGGGTTATGCTGTGAGCTGCGGCTGCGGAAAGCCACGCGCGAC 120
DB 1 AAGCTGAGGCGAAGGGTTATGCTGTGAGCTGCGGCTGCGGAAAGCCACGCGCGAC 120
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QY 361 CAACTCCAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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DB 481 CCGTTCGCGGAGGCGCACTGGGCGATGAGGACAGTGTGACGCGGCGCTGGAGGCGCG 540
QY 541 GGGGCGCTGTAACTGTAGGCGGCTTTTGTGACGAGTG 581

DB 541 GGGGCGCTGTAACTGTAGGCGGCTTTTGTGACGAGTG 581
RESULT 14
LOCUS AX030817 583 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 6 from Patent WO9735971.
ACCESSION AX030817
VERSION AX030817.1 GI:10278311
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
JOURNAL Patent: WO 9735971-A 6 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU)
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
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RLREGNMAVSRVTLTGAVLALVTGAFPAFK"
ORIGIN
Query Match 86.2%; Score 501; DB 6; Length 583;
Best Local Similarity 91.4%; Pred. No. 4e-107;
Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCAAGCTTCAACCCGACACACGCGCTTATGTGGCTGACTTTGTAGCTAT 60
DB 1 ATGGCGACCCCAAGCTTCAACCCGACACACGCGCTTATGTGGCTGACTTTGTAGCTAT 60
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DB 1 AAGCTGAGGCGAAGGGTTATGCTGTGAGCTGCGGCTGCGGAAAGCCACGCGCGAC 120
QY 121 CCGCTGACCAAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 180
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QY 181 TTCTCTGACCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 240
DB 181 TTCTCTGACCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 240
QY 241 CAGGTTTCCGACGAACTTTTCAAGGGGCGCCCAATGGGCGCGCTGTGACCTTCTT 300
DB 241 CAGGTTTCCGACGAACTTTTCAAGGGGCGCCCAATGGGCGCGCTGTGACCTTCTT 300
QY 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAACAAGAAATGAGCTTTGGTGGGA 360
DB 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAACAAGAAATGAGCTTTGGTGGGA 360
QY 361 CAACTCCAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CAACTCCAGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AGTGGCGGCTGGCGGCTTCAAGCTCTTATACGCGGGAAGCGGCGCTTGGAGGACGAC 480
DB 421 AGTGGCGGCTGGCGGCTTCAAGCTCTTATACGCGGGAAGCGGCGCTTGGAGGACGAC 480

Search completed: March 29, 2004, 06:11:59
Job time : 2757.26 secs

QY 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGATGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGATGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTGTAACGTAGAGGGCCCTTTTGTCTAGCAAGTG 581
Db 541 GGGGCCCTGTGTAACGTAGAGGGCCCTTTTGTCTAGCAAGTG 581

RESULT 15
AR020780 579 bp DNA linear PAT 05-DEC-1998
LOCUS AR020780
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION AR020780
VERSION AR020780.1 GI:3975395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 579)
AUTHORS Gustella,J.
TITLE Genes coding for bcl-2 homologues
JOURNAL Patent: US 5789201-A 2 04-AUG-1998;
FEATURES
Location/Qualifiers
1..579
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 85.6%; Score 497.4; DB 6; Length 579;
Best Local Similarity 91.2%; Pred. No. 2.8e-106;
Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCCGACCCAGCCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGCCGACCCAGCCTCGGCCAGACACAGCGCTCTGAGAGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGGCCCGCCGAC 120
Db 61 AAGCTGAGGAGAAAGGTTATGTCTGTGAGCTGGGCTTGGGAAAGGCCCGCCGAC 120
QY 121 CCGGTGACCAAGGCAATGCGGGCTGTGAGAGAGATTGAGACCCGTTCCGCCGAC 180
Db 121 CCACTGACCAAGGCAATGCGGGCTGTGAGAGAGATTGAGACCCGTTCCGCCGAC 180
QY 181 TTCTCTGACCTGGCGGCTACGCTACAGTGACCCAGGCTCAGGCCAGCAAGCTTCACC 240
Db 181 TTCTCTGATCTGGGGCTCAGCTCAGTGAGACCCAGGCTCAGGCCAGCAAGCTTCACC 240
QY 241 CAGGTTTCCAGCAACTTTTCCAAAGGGGGCCCTAATGAGGGCCGTCTTGTGGCACTTT 300
Db 241 CAGGTTTCCAGTGAATCTTTTCCAAAGGGGGCCCAACTGGGGCCGCTTGTAGCTTTT 300
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAGAAATGAGCCTTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCATGAGTGGGA 360
QY 361 CAATGCCAGATTGGATCGTGGCTTACCTGAGAGCAGTCTGGCTGAGCTGGATCCAGC 420
Db 361 CAAATGAGAGATGATGATGCTTACCTGAGAGCGGCTGGCTGAGCTGATCCAGC 420
QY 421 AGTGGGAGCTGGGCGGACTTCAAGCTCTATACGGGGAACGGGGCCCTGAGAGAGCGCGG 480
Db 421 AGTGGGAGCTGGGCGGAGTTCAAGCTCTATACGGGGAACGGGGCCCTGAGAGAGCGCGG 480
QY 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGATGACGGGGCCGTGGCACTG 540
Db 481 CGTCTGCGGAGGAGCACTGGCATGATGAGCAGAGTGATGACGGGGCCGTGGCACTG 540
QY 541 GGGGCCCTGTGTAACGTAGAGGGCCCTTTTGTCTAGCAAG 579
Db 541 GGGGCCCTGTGTAACGTAGAGGGCCCTTTTGTCTAGCAAG 579

CC hypoxanthine ischaemia, human immunodeficiency virus infection or in cell
CC transplants. Up-regulation of the gene can also be used to modify cell
CC lines cultured in vivo, e.g. to develop new lines, to facilitate
CC isolation of hybridomas and to increase survival of primary explants
CC during genetic modification. It can be used to produce recombinant Bcl-2
CC for therapy, diagnosis, antibody production or screening of potential
CC modulators

XX Sequence 581 BP, 105 A, 164 C, 195 G, 117 T, 0 U, 0 Other;

| | | | | | | | |
|-----------------------|----------|--------------|----------|--------|--------|-------|-----|
| Query Match | 581 ; | Score | 581 ; | DB 2 ; | length | 581 ; | |
| Best Local Similarity | 100.0% ; | Prod. No. | 6e-148 ; | | | | |
| Matches | 581 ; | Conservative | 0 ; | Indels | 0 ; | Gaps | 0 ; |

| | | |
|----|--|-----|
| QY | ATGCGCAACCCCACTTCAACCCGAGACAACACGCGCTAGTGGCTGACTTTGTAGGCTAT | 60 |
| Db | 1 ATGCGCAACCCCACTTCAACCCGAGACAACACGCGCTAGTGGCTGACTTTGTAGGCTAT | 60 |
| QY | AGCGTAGAGCAGAAAGGTTATATGTCTGTGAGAGCTGAGGCTGAGGGAAGGCCAGCCGGAC | 120 |
| Db | 61 AGCGTAGAGCAGAAAGGTTATATGTCTGTGAGAGCTGAGGCTGAGGGAAGGCCAGCCGGAC | 120 |
| QY | CCGCTGACCAACCCATATGCGGGGTGTGTGAGACAGATTTGAGACCCCGTTTCCGCGCAC | 180 |
| Db | 121 CCGCTGACCAACCCATATGCGGGGTGTGTGAGACAGATTTGAGACCCCGTTTCCGCGCAC | 180 |
| QY | CCGCTGACCAACCCATATGCGGGGTGTGTGAGACAGATTTGAGACCCCGTTTCCGCGCAC | 240 |
| Db | 121 CCGCTGACCAACCCATATGCGGGGTGTGTGAGACAGATTTGAGACCCCGTTTCCGCGCAC | 240 |
| QY | TTCTCTACCTGGGCGGCTCAGCTACACGTGACCCCAAGGCTCAGCCAGACCAACGCTTACC | 300 |
| Db | 181 TTCTCTACCTGGGCGGCTCAGCTACACGTGACCCCAAGGCTCAGCCAGACCAACGCTTACC | 300 |
| QY | CAGGTTTCCGACGACATTTTCCAAAGGAGGCGCTTAACTGAGGCGCGTCTTGTGACATCTTT | 360 |
| Db | 241 CAGGTTTCCGACGACATTTTCCAAAGGAGGCGCTTAACTGAGGCGCGTCTTGTGACATCTTT | 360 |
| QY | GTCTTTGGGGCTGCGCTGTGTGTGTGAGATGTCAACAAAGAAATGAGACCTTTGGTGGGA | 420 |
| Db | 301 GTCTTTGGGGCTGCGCTGTGTGTGTGAGATGTCAACAAAGAAATGAGACCTTTGGTGGGA | 420 |
| QY | CAAGTCCAGGATTTGAAATCGTGGCTTCCCTGGAGACACGCTGTGGCTGATGGATCCAGAC | 480 |
| Db | 361 CAAGTCCAGGATTTGAAATCGTGGCTTCCCTGGAGACACGCTGTGGCTGATGGATCCAGAC | 480 |
| QY | AGTGGCGGCTGGGCGGACTTCAAGCTCTTAAACGGGGAACGGGCGCTTGGAGAGCGCACG | 540 |
| Db | 421 AGTGGCGGCTGGGCGGACTTCAAGCTCTTAAACGGGGAACGGGCGCTTGGAGAGCGCACG | 540 |
| QY | CGTCTGCGGAGGGGCAACTGGGCGATAGTGAACAAGTGTGACCGGAGGCGCTGGGCACTG | 600 |
| Db | 481 CGTCTGCGGAGGGGCAACTGGGCGATAGTGAACAAGTGTGACCGGAGGCGCTGGGCACTG | 600 |
| QY | GGGGCCCTGGTAACTGATGAGGGGCTTTTGTCTACCAAGTG | 581 |
| Db | 541 GGGGCCCTGGTAACTGATGAGGGGCTTTTGTCTACCAAGTG | 581 |

RESULT 2
AAx25135.
ID AAX25135 standard; DNA; 581 BP.

DT 05-JUL-1999 (first entry)

DE Mouse bcl-w gene derivative.

KW Spermatogenesis; bcl-3 gene; mouse; fertility; infertility;

KW animal model; ss.

XX

Mus sp.

[illegible]

key
CDs
ET
ET

FT : 33

XX
FN MO9913710-A1
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU000764.
XX
PF 16-SEP-1997; 97AU-0009228.
XX
PR
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

Only S. Adams J, Print C, Gibson L, Koentgen F;
WPI: 1999-243890/20.
P-PSDB; AA105533.
An animal model exhibiting reduced levels of a Bcl-w protein and/or
protein associated with Bcl-w.
Disclosure: Page 38; 52pp; English.

The present sequence is described as a derivative of the mouse *bcl-w* gene (see AAX55133) and encodes Bcl-w protein (see AAY05533), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation in at least one allele of the human or murine *bcl-w* gene or in a gene associated with *bcl-w*. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.

| | |
|---------------------------|--|
| 80 | Sequence 581 BP; 105 A; 164 C; 125 G; 117 T; 0 U; 0 Other; |
| Query Match | 100.0%; Score 581; DB 2; Length 581; |
| Best Local Similarity | 100.0%; Pred. No. 6e-148; |
| Matches 581; Conservative | 0; Mismatches 0; Indels 0; Gaps 0 |

| | | | |
|----|-----|---|-----|
| QY | 1 | ATGCGAACCAGGCTCAACCCATACACACGCGCTCAAGGCTGACTTTGTAGGCTAT | 60 |
| Db | 1 | ATGCCAGCCCGAGCTCAACCCCAACACACGCGCTCAAGGCTAT | 60 |
| QY | 61 | AGGCTAGGACAGAAAGGTTATGTCTGTAGACTGGGCTCGGGAGAGGCCAGCGCGGAC | 120 |
| Db | 61 | AGGCTAGGACAGAAAGGTTATGTCTGTAGACTGGGCTCGGGAGAGGCCAGCGCGGAC | 120 |
| QY | 121 | CCGCTGCACCAAGCATGGGCGCTCTGGAGACGAGTTTGAGACCGCTTTCCGCGCAC | 180 |
| Db | 121 | CCGCTGCACCAAGCATGGGCGCTCTGGAGACGAGTTTGAGACCGCTTTCCGCGCAC | 180 |
| QY | 181 | TTCTCTGACTGCGCGCTACGCTACACGTGACCCCAAGGCTCAGCCACGACCGTTTACC | 240 |
| Db | 181 | TTCTCTGACTGCGCGCTACGCTACACGTGACCCCAAGGCTCAGCCACGACCGTTTACC | 240 |
| QY | 241 | CAGGTTCCGACGAACTTTCCAAAGGGGCGCTTAACTGGGCGCTCTTGTGGCACTTTT | 300 |
| Db | 241 | CAGGTTCCGACGAACTTTCCAAAGGGGCGCTTAACTGGGCGCTCTTGTGGCACTTTT | 300 |
| QY | 301 | GTTTTGGGGGCGCCCTGTGTGCTGAGGTGTCAAAAGAAATGAGACCTTTGTGTGGGA | 360 |
| Db | 301 | GTTTTGGGGGCGCCCTGTGTGCTGAGGTGTCAAAAGAAATGAGACCTTTGTGTGGGA | 360 |
| QY | 361 | CAAGTCACAGATTGAGTGTGGCTTAAGCTGAGACACGTCGTGGCTGACTGATTCACAGC | 420 |
| Db | 361 | CAAGTCACAGATTGAGTGTGGCTTAAGCTGAGACACGTCGTGGCTGACTGATTCACAGC | 420 |
| QY | 421 | AGTGGCGGTGGGCGGCACTTCAAGCTTATACGGGGACGGGGCGCTGAGAGACGCAAG | 480 |

Db 421 AGTGGCGCTGGCGGACTTCACAGCTTATACGCGGACCGGCGCTTGAGGACGACCG 480
Qy 481 CGTCTCGGGAGGGCAACTGGGCGATGAGTGAAGACAGTGTGACCGGGGCGCTGGACTG 540
Db 481 CGTCTCGGGAGGGCAACTGGGCGATGAGTGAAGACAGTGTGACCGGGGCGCTGGACTG 540
Qy 541 GGGGCGCTGGTAACTGTAGAGGGGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCGCTGGTAACTGTAGAGGGGCTTTTGTGTAGCAAGTG 581

RESULT 3
AAK25133
ID AAK25133 standard; DNA; 581 BP.
XX
AC AAK25133;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse bcl-w gene.
XX
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
XX
OS Mus sp.
XX
PN MO913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98MO-AU000764.
XX
PR 16-SEP-1997; 97AU-00009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX
DR WPI; 1999-243890/20.
DR P-PSDB; AAY05531.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX protein associated with Bcl-w.
PS Claim 3; Page 34; 52pp; English.
XX
CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see
CC AAY05531), a pro-survival member of the Bcl-2 family which is widely
CC expressed and which is essential for spermatogenesis. The invention
CC relates generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for inducing or
CC reducing fertility of male animals. Methods are provided for the
CC treatment of infertility, or for reducing fertility, by modulating
CC spermatogenesis. An animal model carries a mutation in at least one
CC allele of the human or murine bcl-w gene or in a gene associated with bcl
CC -w. Such animals have disorganised seminiferous tubules and are
CC substantially infertile, but possess no other major abnormalities as
CC determined by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of inducing,
CC enhancing or otherwise facilitating spermatogenesis in animals, or which
CC can induce infertility
SQ Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 U; 0 Other;

Query Match 96.4%; Score 560.2; DB 2; Length 581;
Best Local Similarity 97.8%; Pred. No. 2.7e-142;
Matches 568; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ATGCCGACCCGACCTTCACACCCGACACACCGGCTCTAGTGGCTGACTTTGTAGCTAT 60
Db 1 ATGGGACCCCGACCTTCACACCCGACACACCGGCTCTAGTGGCTGACTTTGTAGCTAT 60
Qy 61 AGGCTGAGGCAAGAGGTATGTCTGTGAGCTGGGCGTGGGGAAGGCCCGCGCGAC 120

Db 61 AAGCTGAGGCAAGAGGTATGTCTGTGAGCTGGGCGTGGGGAAGGCCCGCGCGAC 120
Qy 121 CGGCTGACCAAGCCATGCGGGCTGTGTGAGACGAGTGTAGACCGCTTTCCGCGGACC 180
Db 121 CGGCTGACCAAGCCATGCGGGCTGTGTGAGACGAGTGTAGACCGCTTTCCGCGGACC 180
Qy 181 TTCTGTACCTGGGCGGCTCAGCTACAGTACCCCAAGCTCAGGCCAGCAAGCTTACC 240
Db 181 TTCTGTACCTGGGCGGCTCAGCTACAGTACCCCAAGCTCAGGCCAGCAAGCTTACC 240
Qy 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTCCTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCTTAACTGGGCGCTTGTGGCATTCCTT 300
Qy 301 GTCTTTGGGCGTGGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 360
Db 301 GTCTTTGGGCGTGGCGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGCCCTTTGTGGGA 360
Qy 361 CAAGTCCAGATTTGATCTGTGCTTACCTGGAAGACAGTCTGCTGATGATCCAGAC 420
Db 361 CAAGTCCAGATTTGATCTGTGCTTACCTGGAAGACAGTCTGCTGATGATCCAGAC 420
Qy 421 AGTGGCGGCTGGGCGGACTTCACAGCTTATACGCGGACCGGCGCTTGAGGACGACCG 480
Db 421 AGTGGCGGCTGGGCGGACTTCACAGCTTATACGCGGACCGGCGCTTGAGGACGACCG 480
Qy 481 CGTCTGCGGAGGCAACTGGGCGATGAGTGAAGACAGTGTGACGGGGCGCTGGGACTG 540
Db 481 CGTCTGCGGAGGCAACTGGGCGATGAGTGAAGACAGTGTGACGGGGCGCTGGGACTG 540
Qy 541 GGGGCGCTGGTAACTGTAGAGGGGCTTTTGTGTAGCAAGTG 581
Db 541 GGGGCGCTGGTAACTGTAGAGGGGCTTTTGTGTAGCAAGTG 581

RESULT 4
ADB52996
ID ADB52996 standard; DNA; 582 BP.
XX
AC ADB52996;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; ds.
OS Rattus norvegicus.
XX
PN WO2003065993-A2.
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003MO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363549P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.
 PR 04-SEP-2002; 2002US-0407688P.
 PR 28-JAN-2003; 2003US-0442900P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
 PI Elashoff M;
 XX
 DR WPI; 2003-731472/69.
 XX
 PT Determining if a compound induces a toxic effect on a tissue or cell, for
 PT identifying hepatotoxic compounds, comprises comparing a gene expression
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
 PT mean values.
 XX
 PS Claim 44; SEQ ID NO 3538; 874bp; English.
 XX
 CC The present invention describes a method for determining whether a
 CC compound induces a toxic effect on a tissue or cell. The method comprises
 CC preparing a gene expression profile of a tissue or cell sample exposed to
 CC the compound, and comparing the gene expression profile to a database
 CC comprising data or information on the Tox mean and non-Tox mean value.
 CC The method is useful for predicting or identifying at least one toxic
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The
 CC genes listed in the specification are useful as diagnostic or toxicity
 CC markers for the prediction or identification of the physiological state
 CC of tissue or cell sample that has been exposed to a compound, or to
 CC identify or predict the toxic effects of a compound or an agent. These
 CC may also be used as markers for monitoring toxicity progression or for
 CC drug screening. The present sequence represents a primary rat hepatocyte
 CC toxicity modelling related gene sequence from the present invention.
 XX
 SQ Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;
 Query Match 93.7%; Score 544.2; DB 9; Length 582;
 Best Local Similarity 96.0%; Pred. No. 6.1e-138;
 Matches 558; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 ATGCGCAGCCCGAGCTTCAACCCAGACACAGCGCTCTAGTGGCTAT 60
 DB 1 ATGCGCAGCCCGAGCTTCAACCCAGACACAGCGCTCTAGTGGCTAT 60
 QY 61 AGGCTGAGGAGAGAGGTTATGCTGTGAGCTGGGCTGGGAGGCCAGCGCGAC 120
 DB 61 AGGCTGAGGAGAGAGGTTATGCTGTGAGCTGGGCTGGGAGGCCAGCGCGAC 120
 QY 121 CCGCTGACCAAGCATGCGGGCTGCTGAGACGAGAGTTTGAAGCCGTTCCGCCGAC 180
 DB 121 CCGCTGACCAAGCATGCGGGCTGCTGAGACGAGAGTTTGAAGCCGTTCCGCCGAC 180
 QY 181 TTCTCTGACCTGGCGGCTGACGTAACAGTACCCAGCGCTCAAGCCAGCAACGCTTAC 240
 DB 181 TTCTCTGACCTGGCGGCTGACGTAACAGTACCCAGCGCTCAAGCCAGCAACGCTTAC 240
 QY 241 CAGGTTCCAGCAACCTTTTCCAAAGGGGGCCCTTAATCTGGGGCCGCTTGTGGATCTTT 300
 DB 241 CAGGTTCCAGCAACCTTTTCCAAAGGGGGCCCTTAATCTGGGGCCGCTTGTGGATCTTT 300
 QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
 DB 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTCAACAAAGAAATGAGACCTTTGGTGGGA 360
 QY 361 CAAGTCCAGGATTGATCTGGCTTACTGTGAGACAGCTGTGGCTGATGATGATCCACAG 420
 DB 361 CAAGTCCAGGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AGTGGCGGCTGGGGGAGCTTCAACAGCTTATAGGGGAGCGGGCCCTGAGAGAGCGAC 480
 DB 421 AGTGGCGGCTGGGGGAGCTTCAACAGCTTATAGGGGAGCGGGCCCTGAGAGAGCGAC 480
 QY 481 CGTGTGGGAGAGGAGCACTGGGCAATGATGAGACAGTGTGTGGGGCCGCTGGGACATG 540

DB 481 CGTGTGGGAGAGGAGCACTGGGCAATGATGAGACAGTGTGTGGGGCCGCTGGGACATG 540
 QY 541 GGGGCGCTGGTAACTAGTAGGGGCTTTTGTGTAAGAGT 581
 DB 541 GGGGCGCTGGTAACTAGTAGGGGCTTTTGTGTAAGAGT 581
 RESULT 5
 AAV28333
 ID AAV28333 standard; cDNA; 579 BP.
 XX
 AC AAV28333;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Rat bcl-y gene.
 XX
 KM ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
 XX
 OS Rattus sp.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 1..579
 FT /*tag= a
 FT /product= "bcl-y"
 FT /note= "No stop codon given"
 XX
 PN US5789201-A.
 XX
 PD 04-AUG-1998.
 XX
 PF 11-FEB-1997; 97US-00798897.
 XX
 PR 23-FEB-1996; 96US-0012201P.
 XX
 PA (COCE-) COCENSYS INC.
 XX
 PI Guastella J;
 XX
 DR WPI; 1998-446079/38.
 XX
 DR P-PSDB; AAM61391.
 XX
 PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
 PT recombinant protein for use in treating uncontrolled cell growth e.g.
 PT cancers.
 XX
 PS Claim 2; Column 13/14; 27pp; English.
 XX
 CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
 CC family. components in the cell death pathway. The bcl-2 family has both
 CC apoptotic activity and the apoptosis blocking activity. bcl-y falls in
 CC the apoptosis activity category. The recombinant protein may be used to
 CC prevent uncontrolled cell growth, either by its direct administration to
 CC recombinant genetic constructs to increase its expression in vivo. Also,
 CC antisense constructs can be used in disorders where prevention of cell
 CC death is desired
 XX
 SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
 Query Match 93.0%; Score 540.6; DB 2; Length 579;
 Best Local Similarity 95.9%; Pred. No. 5.8e-137;
 Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 ATGCGACCCAGCCTCAACCCAGACACAGCGCTAGTGGCTGACTTTGATGAGTAT 60
 DB 1 ATGCGACCCAGCCTCAACCCAGACACAGCGCTAGTGGCTGACTTTGATGAGTAT 60
 QY 61 AGGCTGAGGAGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
 DB 61 AGGCTGAGGAGAGAGGTTATGCTGTGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120
 QY 121 CCGCTGACCAAGCATGCGGGCTGCTGAGAGACAGATTGAGACCCGTTCCGCCGAC 180

Db 121 CCGCTGACCAAGCCATGCGGGGAGAGACAGATTGAGACCCCGCTTCGGGGCCACC 180
QY 181 TTCTCTGACCTGGCGCGCTCAGCTACAGCTGAGACCCAGGCTCAGCCAGCAAGCTTACCC 240
Db 181 TTCTCTGACCTGGCGCGCTCAGCTACAGCTGAGACCCAGGCTCAGCCAGCAAGCTTACCC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCCCTAACTGGGGCCGCTTTGGCATTTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCCCTAACTGGGGCCGCTTTGGCATTTCTT 300
QY 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGGTGGGA 360
QY 361 CAACTCAGGATTTGATTCGTGAGCTTACCTGAGACAGCTCTGCTGACTGATCCAGAC 420
Db 361 CAACTCAGGATTTGATTCGTGAGCTTACCTGAGACAGCTCTGCTGACTGATCCAGAC 420
QY 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTAATACGGGGACGGGGCCCTGAGAGACGACGG 480
Db 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTAATACGGGGACGGGGCCCTGAGAGACGACGG 480
QY 481 CGTCTGCGGGAGGGGAACTGGGCACTAGAGAGACAGTGTCTGACGGGGGCTGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCACTAGAGAGACAGTGTCTGACGGGGGCTGTGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAG 579
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAG 579

RESULT 6
AA15945
ID AA15945 standard; cDNA; 579 BP.
AC AA15945;
XX
XX 20-MAY-1999 (first entry)
DE cDNA encoding the rat bcl-y protein.
XX
XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
ss.
XX
OS Rattus sp.
XX
PN US883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COGENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR P-PsDB; AA97391.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX modulating programmed cell death.
XX
PS Disclosure; Col 13-16; 26pp; English.
XX

CC The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 U; 0 Other;
Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 5.8e-137;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 ATGCCGACCCAGCCTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGGCTAT 60
Db 1 ATGCCGACCCAGCCTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGAGGCTAT 60
QY 61 AAGCTGAGAGAGAAAGGTTATGTCTGAGAGCTGGGCTGGGAGAGCCGCGAC 120
Db 61 AAGCTGAGAGAGAAAGGTTATGTCTGAGAGCTGGGCTGGGAGAGCCGCGAC 120
QY 121 CCGCTGACCAAGGCAATGCGGGGCTGTGAGAGAGAGTTTGAACCCGTTCCGCGCAC 180
Db 121 CCGCTGACCAAGGCAATGCGGGGCTGTGAGAGAGAGTTTGAACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCGCGCTCAGCTACAGTGAACCCAGGCTCAAGCCAGCAAGCTTACCC 240
Db 181 TTCTCTGACCTGGCGCGCTCAGCTACAGTGAACCCAGGCTCAAGCCAGCAAGCTTACCC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCCCTAACTGGGGCCGCTTTGGGATTTCTT 300
Db 241 CAGGTTCCGACGAACTTTTCCAAAGGGGCGCCCTAACTGGGGCCGCTTTGGGATTTCTT 300
QY 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGGTGGGA 360
Db 301 GTCTTTGGGGCTCCCTGTGTGCTGAGAGTCAAGAAATGAGAGCTTTGGTGGGA 360
QY 361 CAACTCAGGATTTGATTCGTGAGCTTACCTGAGACAGCTCTGCTGACTGATCCAGAC 420
Db 361 CAACTCAGGATTTGATTCGTGAGCTTACCTGAGACAGCTCTGCTGACTGATCCAGAC 420
QY 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTAATACGGGGACGGGGCCCTGAGAGACGACGG 480
Db 421 AGTGGCGGCTGGGGGAGCTTCAAGCTCTAATACGGGGACGGGGCCCTGAGAGACGACGG 480
QY 481 CGTCTGCGGGAGGGGAACTGGGCACTAGAGAGACAGTGTCTGACGGGGGCTGTGGCACTG 540
Db 481 CGTCTGCGGGAGGGGAACTGGGCACTAGAGAGACAGTGTCTGACGGGGGCTGTGGCACTG 540
QY 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAG 579
Db 541 GGGGCCCTGTGTAAGTGTAGGGGCTTTTGTGCTAGCAG 579

RESULT 7
ABV78153
ID ABV78153 standard; DNA; 582 BP.
AC ABV78153;
XX
XX 15-NOV-2002 (first entry)
DT

```
XX Human bcl-w DNA SEQ ID NO 37.
DE
XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KM
XX vitruicide; protozoacide; gene; ds.
OS
XX Homo sapiens.
PN
XX WO200255693-A2.
PD
XX 18-JUL-2002.
PF
XX 09-JAN-2002; 2002WO-EP000152.
PR
XX 09-JAN-2001; 2001DE-01000586.
PR
XX 26-OCT-2001; 2001DE-01055280.
PR
XX 29-NOV-2001; 2001DE-01058411.
PR
XX 07-DEC-2001; 2001DE-01060151.
PA
XX (RIBO-) RIBOPHARMA AG.
PI
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
XX oncogenes, by administering double-stranded RNA complementary to the
XX target and having an overhang.
XX
PS Claim 10; Page 134; 203pp; German.
XX
XX The invention relates to inhibiting expression of a target gene (I) in a
XX cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
XX structure of at most 49 consecutive bases. At least part of one strand
XX (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
XX has an overhang of 1-4 nucleotides. The method is used to inhibit the
XX expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
XX in humans, also genes in plasmodium or in viruses or viroids that are
XX pathogenic for humans, animals or plants. Introducing an overhang into
XX dsRNA greatly increases effectiveness for inhibiting gene expression.
XX both in vivo and in vitro and also increases stability and thus the
XX effective concentration inside the cell. The present sequence is that of
XX a gene related to the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
Query Match 87.1%; Score 505.8; DB 6; Length 582;
Best Local Similarity 91.9%; Pred. No. 1,7e-127;
Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 ATGCCGACCCCGAGCTCAACCCGACACACGCGCTTACGAGGCTTGAAGGCTAT 60
DB 1 ATGCCGACCCCGAGCTTGGCCCGACACACGCGCTTGGTGGACCTTTGAGGCTTAT 60
QY 61 AGGCTGAGGACGAGGCTTATCTGTGAGCTGGGCTGGGAGAGGCCGACGCGCGAC 120
DB 61 AAGCTGAGGACGAGGCTTATCTGTGAGCTGGGCTGGGAGAGGCCGACGAGCTGAC 120
QY 121 CCGCTGACACCAAGCCATGCGGCGCTGTGAGACGAGTTTGAAGCCGTTCCCGCGAC 180
DB 121 CCGCTGACACCAAGCCATGCGGCGCTGTGAGATGATTCAGACCCGCTTCCGCGAC 180
QY 121 CCGCTGACACCAAGCCATGCGGCGCTGTGAGATGATTCAGACCCGCTTCCGCGAC 180
DB 121 CCGCTGACACCAAGCCATGCGGCGCTGTGAGATGATTCAGACCCGCTTCCGCGAC 180
QY 181 TTCTCTAATCTGGCGCTCAGCTCAGTGAATGATTCAGACCCGCTTCCGCGAC 240
DB 181 TTCTCTAATCTGGCGCTCAGCTCAGTGAATGATTCAGACCCGCTTCCGCGAC 240
QY 181 TTCTCTAATCTGGCGCTCAGCTCAGTGAATGATTCAGACCCGCTTCCGCGAC 240
DB 181 TTCTCTAATCTGGCGCTCAGCTCAGTGAATGATTCAGACCCGCTTCCGCGAC 240
QY 241 CAGGTTCCGACGAACTTTTTCAGAGGCGGCGCTTACCTGAGGCGCTTTGGGATCTTT 300
DB 241 CAGGTTCCGACGAACTTTTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 301 GTCTTTGGGCGTGGCTGTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGG 360
DB 301 GTCTTTGGGCGTGGCTGTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGG 360
301 GTCTTTGGGCGTGGCTGTGTGTGTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGG 360
```

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QY 361 CAACTCCAGAAATTGATCGTGCCCTACCTGAGACACGCTGTGCTGACTGATCCACAGC 420
DB 361 CAACTCCAGAAATTGATCGTGCCCTACCTGAGACACGCGGCTGCTGACTGATCCACAGC 420
QY 421 AGTGCGGCTGGGCGGAGCTTCAAGCTTATACCGGAGACGCGGCGGCTGAGACGCAAG 480
DB 421 AGTGCGGCTGGGCGGAGCTTCAAGCTTATACCGGAGACGCGGCGGCTGAGACGCGG 480
QY 481 CGTCTGCGGAGAGGCACTGGGCACTGAGTGAACAGAGTGTGAGCGGCGGCGTGGCACTG 540
DB 481 CGTCTGCGGAGAGGCACTGGGCACTGAGTGAACAGAGTGTGAGCGGCGGCGTGGCACTG 540
QY 541 GGGGCGGCTGTACTGTATGAGGCGGCTTTTCTGTGCAAGT 581
DB 541 GGGGCGGCTGTACTGTATGAGGCGGCTTTTCTGTGCAAGT 581
RESULT 8
ABZ35729
ID ABZ35729 standard; DNA; 582 BP.
XX
XX ABZ35729;
AC
XX
XX 07-FEB-2003 (first entry)
DT
XX
XX Human bcl-w polynucleotide SEQ ID NO 37.
DE
XX
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; vitruicide;
XX protozoacide; gene expression; antisense; tumour; infection; plasmodium;
XX virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
XX Hepatitis C virus; human papilloma virus; gene; ds.
XX
XX Homo sapiens.
OS
XX DE10100586-A1.
PN
XX 18-JUL-2002.
PD
XX 09-JAN-2001; 2001DE-01000586.
PF
XX 09-JAN-2001; 2001DE-01000586.
PR
XX 09-JAN-2001; 2001DE-01000586.
XX
XX (RIBO-) RIBOPHARMA AG.
PA
XX
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
PI
XX
XX WPI; 2002-683450/74.
XX
XX Inhibiting expression of target genes, useful e.g. for treating tumours,
XX by introducing into cells two double-stranded RNAs that are complementary
XX to the target.
XX
PS Claim 13; Page 30-31; 100pp; German.
XX
XX The invention relates to inhibiting expression of a target gene in a cell
XX by introducing at least two oligonucleotides (dsRNA1 and II), both
XX with a double-stranded (ds) structure of at most 49 sequential nucleotide
XX pairs. At least part of one strand (S1, S2) of the ds structures in each
XX of dsRNA1 and II are complementary to regions in the target gene. The
XX method uses antisense inhibition of gene expression using double stranded
XX RNA inhibition (RNAi). The method is particularly used to treat tumours
XX or infections, especially by plasmodium or viruses/viroids (pathogenic on
XX humans, animals or plants). The method provides more effective inhibition
XX of expression than known methods using a single dsRNA, even at very low
XX concentrations. When dsRNA has at least one unpaired nucleotide at the
XX end, stability (and thus effective concentration in the cell) is improved
XX and efficiency can be increased further by pretreating the cells with
XX interferon. The present sequence is that of a target DNA of the invention
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;
Query Match 87.1%; Score 505.8; DB 6; Length 582;
```

Best Local Similarity 91.9%; Pred. No. 1.7e-127; Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
QY 1 ATGCCGACCCCAAGCTTCAACAGCCAGACAGAGCTGATGAGCTTTAGAGCTAT 60
DB 1 ATGGGACCCCAAGCTTCAAGCCAGACAGAGCTTGTGAGACTTTGTAGTTAT 60
QY 61 AGCTGAGGACAGAGGTTATGCTGTGAGAGCTGAGGAGGAGCCAGCCGAC 120
DB 61 AAGCTGAGGACAGAGGTTATGCTGTGAGAGCTGAGGAGGAGCCAGCACTAC 120
QY 121 CCGCTGACCAAGCCAGCTGAGGAGCTGAGAGCAAGTTGAGACCCGTTCCGCGAC 180
DB 121 CCGCTGACCAAGCCAGCTGAGGAGCTGAGAGATGAGTTGAGACCCGTTCCGCGAC 180
QY 181 TTCTGACCTGAGCCGCTGAGCTACAGCTGACAGCCAGGCTACGCCAGCAAGCTTAC 240
DB 181 TTCTGATCTGAGCCGCTGAGCTACAGCTGACAGCCAGGCTACGCCAGCAAGCTTAC 240
QY 241 CAGCTTCCGACGAACTTTTCAAGGAGGAGCCCTAAGTGGGAGCTTTGTGAGCTTT 300
DB 241 CAGCTTCCGACGAACTTTTCAAGGAGGAGCCCAAGTGGGAGCTTTGTAGCTTTT 300
QY 301 GTCTTTGGGAGCTGAGCTGTGTGAGAGCTGACAAAGAAATGAGCTTTGTGAGGA 360
DB 301 GTCTTTGGGAGCTGAGCTGTGTGAGAGCTGACAAAGAAATGAGAACTGTTGAGGA 360
QY 361 CAACTCAGAGATTTGATGCTGAGCTGAGAGCAAGCTTGTGAGCTGATCCAGAC 420
DB 361 CAACTCAGAGATTTGATGCTGAGCTGAGAGCAAGCTTGTGAGCTGATCCAGAC 420
QY 421 AGTGGAGGCTGAGGAGCTTCAAGCTTATAGGAGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 AGTGGAGGCTGAGGAGCTTCAAGCTTATAGGAGAGGAGGAGGAGGAGGAGGAGG 480
QY 481 CGCTGAGGAGGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 GGGGCGCTGTAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 581
DB 541 GGGGCGCTGTAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 581
```

RESULT 9
ABX09972
ID ABX09972 standard; DNA; 582 BP.

XX
AC ABX09972;

XX
DT 23-JAN-2003 (first entry)

XX
DE Human bcl-2 DNA fragment SEQ ID 37.

XX
KW Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;
prion; inhibition; human; ds.

XX
OS Homo sapiens.

XX
PN DE10100587-C1.

XX
PD 21-NOV-2002.

XX
PF 09-JAN-2001; 2001DE-01000587.

XX
PR 09-JAN-2001; 2001DE-01000587.

XX
PA (RIBO-) RIBOPHARMA AG.

XX
PI Kreutzler R, Limmer S, Rost S, Hadwiger P;

XX
DR WPI; 2002-742209/81.

PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.

XX
PS Disclosure; Page 35-36; 98pp; German.

CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the target gene at
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with
CC the target gene and the cells are treated with interferon before
CC introduction of dsRNA. The method is used to inhibit expression of
CC target genes, particularly oncogenes, cytokine genes, id (not defined)
CC protein genes; developmental or prion genes, or genes expressed in
CC pathogenic organisms (particularly plasmids) or in viruses or viroids
CC (pathogenic in humans, animals or plants). Treating the cells with
CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC gene fragments used to illustrate the method of the invention

XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 U; 0 Other;

Query Match 87.1%; Score 505.8; DB 6; Length 582;

Best Local Similarity 91.9%; Pred. No. 1.7e-127; Matches 534; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
QY 1 ATGCCGACCCCAAGCTTCAACAGCCAGACAGAGCTGATGAGCTTTAGAGCTAT 60
DB 1 ATGGGACCCCAAGCTTCAAGCCAGACAGAGCTTGTGAGACTTTGTAGTTAT 60
QY 61 AGCTGAGGACAGAGGTTATGCTGTGAGAGCTGAGGAGGAGCCAGCCGAC 120
DB 61 AAGCTGAGGACAGAGGTTATGCTGTGAGAGCTGAGGAGGAGCCAGCACTAC 120
QY 121 CCGCTGACCAAGCCAGCTGAGGAGCTGAGAGCAAGTTGAGACCCGTTCCGCGAC 180
DB 121 CCGCTGACCAAGCCAGCTGAGGAGCTGAGAGCAAGTTGAGACCCGTTCCGCGAC 180
QY 181 TTCTGACCTGAGCCGCTGAGCTACAGCTGACAGCCAGGCTACGCCAGCAAGCTTAC 240
DB 181 TTCTGATCTGAGCCGCTGAGCTACAGCTGACAGCCAGGCTACGCCAGCAAGCTTAC 240
QY 241 CAGCTTCCGACGAACTTTTCAAGGAGGAGCCCTAAGTGGGAGCTTTGTGAGCTTT 300
DB 241 CAGCTTCCGACGAACTTTTCAAGGAGGAGCCCAAGTGGGAGCTTTGTAGCTTTT 300
QY 301 GTCTTTGGGAGCTGAGCTGTGTGAGAGCTGACAAAGAAATGAGCTTTGTGAGGA 360
DB 301 GTCTTTGGGAGCTGAGCTGTGTGAGAGCTGACAAAGAAATGAGAACTGTTGAGGA 360
QY 361 CAACTCAGAGATTTGATGCTGAGCTGAGAGCAAGCTTGTGAGCTGATCCAGAC 420
DB 361 CAACTCAGAGATTTGATGCTGAGCTGAGAGCAAGCTTGTGAGCTGATCCAGAC 420
QY 421 AGTGGAGGCTGAGGAGCTTCAAGCTTATAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 AGTGGAGGCTGAGGAGCTTCAAGCTTATAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 481 CGCTGAGGAGGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 GGGGCGCTGTAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 581
DB 541 GGGGCGCTGTAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 581
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RESULT 10
ABL91694
ID ABL91694 standard; DNA; 582 BP.

| | | | | | | | | | | | | | | | | | | |
|-----------|---|--|--------------------------|-----------------------|--------------|-------------|-----|--|--|--|--|--|--|--|--|--|--|--|
| Db | 301 | GTCTTTGGGGCTGCAC | TGTGTGCTGAGAGTGTCAAA | GAGAGTGGAA | CCGATGGTGGGA | 360 | | | | | | | | | | | | |
| Qy | 361 | CAAGTCACAGATTGA | TGATGCTGGCCCTTA | CCGTGGAGACAGT | CGTGGTGA | CTGGATCCAGC | 420 | | | | | | | | | | | |
| Db | 361 | CAAGTCACAGAGTGA | TGTGTGCTTACCTCGAGAG | CGCGCTGGCTTGA | CTGGATCCAGC | 420 | | | | | | | | | | | | |
| Qy | 421 | AGTGGCGGCTGGGCGG | ACCTTCACAGCTCTATACCGG | GCACGGGCGCTGGAGACGC | ACGCGG | 480 | | | | | | | | | | | | |
| Db | 421 | AGTGGGGGCTGGGCGG | AGTTTCACACCTCTAATACGGG | ACCGGGCCCTGGAGAGCGCGG | 480 | | | | | | | | | | | | | |
| Qy | 481 | CGTCTCGGAGAGGGG | CAACTGTCATGAGACACAGTGTG | ATCGGGGGCCGTGGCACTG | 540 | | | | | | | | | | | | | |
| Db | 481 | CGTCTCGGAGAGGGG | CAACTGTCATGAGAGACAGTGTG | ATCGGGGGCCGTGGCACTG | 540 | | | | | | | | | | | | | |
| Qy | 541 | GGGGCCCTGGTAACTG | TAGGGCCCTTTTGTGTAGCAAGT | 581 | | | | | | | | | | | | | | |
| Db | 541 | GGGGCCCTGGTAACTG | TAGGGGACCTTTTGTGTAGCAAGT | 581 | | | | | | | | | | | | | | |
| RESULT 11 | | | | | | | | | | | | | | | | | | |
| AAx25132 | ID | AAx25132 | standard; DNA; 581 BP. | | | | | | | | | | | | | | | |
| AAx25132; | AC | | | | | | | | | | | | | | | | | |
| XX | 05-JUL-1999 | (first entry) | | | | | | | | | | | | | | | | |
| XX | DE | Human bcl-w gene. | | | | | | | | | | | | | | | | |
| XX | DE | Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; | | | | | | | | | | | | | | | | |
| XX | XX | animal model; ss. | | | | | | | | | | | | | | | | |
| OS | Homo sapiens. | | | | | | | | | | | | | | | | | |
| FN | MO9913710-A1. | | | | | | | | | | | | | | | | | |
| PD | 25-MAR-1999. | | | | | | | | | | | | | | | | | |
| PF | 16-SEP-1998; | 98MO-AU000764. | | | | | | | | | | | | | | | | |
| PR | 16-SEP-1997; | 97AU-00009228. | | | | | | | | | | | | | | | | |
| PA | (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. | | | | | | | | | | | | | | | | | |
| PI | Cory S, Adams J, Print C, Gibson L, Koentgen F; | | | | | | | | | | | | | | | | | |
| DR | WPI; 1999-243890/20. | | | | | | | | | | | | | | | | | |
| PT | P-PSDB; AAY05530. | | | | | | | | | | | | | | | | | |
| PS | An animal model exhibiting reduced levels of a Bcl-w protein and/or | | | | | | | | | | | | | | | | | |
| XX | protein associated with Bcl-w. | | | | | | | | | | | | | | | | | |
| XX | Claim 3; Page 32; 52pp; English. | | | | | | | | | | | | | | | | | |
| CC | The present sequence is the human bcl-w gene encoding Bcl-w protein (see | | | | | | | | | | | | | | | | | |
| CC | AAV05530), a pro-survival member of the Bcl-2 family which is widely | | | | | | | | | | | | | | | | | |
| CC | expressed and which is essential for spermatogenesis. The invention | | | | | | | | | | | | | | | | | |
| CC | relates generally to a method of treatment and to an animal model for the | | | | | | | | | | | | | | | | | |
| CC | identification of molecules and genetic sequences useful for inducing or | | | | | | | | | | | | | | | | | |
| CC | reducing fertility of male animals. Methods are provided for the | | | | | | | | | | | | | | | | | |
| CC | treatment of infertility, or for reducing fertility, by modulating | | | | | | | | | | | | | | | | | |
| CC | spermatogenesis. An animal model carries a mutation is at least one | | | | | | | | | | | | | | | | | |
| CC | allele of the human or murine bcl-w gene or in a gene associated with bcl-w | | | | | | | | | | | | | | | | | |
| CC | -w. Such animals have disorganized seminiferous tubules and are | | | | | | | | | | | | | | | | | |
| CC | substantially infertile, but possess no other major abnormalities as | | | | | | | | | | | | | | | | | |
| CC | determined by histological examination. They can be used to screen for | | | | | | | | | | | | | | | | | |
| CC | therapeutic molecules including genetic sequences capable of inducing, | | | | | | | | | | | | | | | | | |
| CC | enhancing or otherwise facilitating spermatogenesis in animals, or which | | | | | | | | | | | | | | | | | |
| CC | can induce infertility | | | | | | | | | | | | | | | | | |
| XX | | | | | | | | | | | | | | | | | | |
| XX | Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other; | | | | | | | | | | | | | | | | | |

Query Match 86.5%; Score 502.6; DB 2; Length 581;
 Best Local Similarity 91.6%; Pred. No. 1,2e-126;
 Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```

QY 1 ATGCCGACCCGAGCTCAACCCAGACACAGCGCTTACTAGCTCACTTTGAGGCTAT 60
DB 1 ATGGCGACCCGAGCTTGGCCCGACACACGCGCTTGTGGACACTTTGAGGTTAT 60
QY 61 AGCGTAGAGCAGAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGGCCAGCGCCGAC 120
DB 61 AAGCTAGAGCAGAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGGCCAGCGCTGAC 120
QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGAGACAGAGTTTGAACCCGTTCCGCGCAC 180
DB 121 CCGCTGACCAAGCCATGCGGGCAGCTGAGATGAGTTGAGACCCGCTTCCGCGCAC 180
QY 181 TTCTCTGACTGGCCGCTCAGCTACACAGTACCCCGAGCTCAAGCCAGACGCTTAC 240
DB 181 TTCTCTGATCTGGCGCTCAGCTACAGTACCCCGAGCTCAAGCCAGACGCTTAC 240
QY 241 CAGGTTCCGACGAACTTTTCCAAAGGGGGCCCTAAGTGGGGCCGCTTGGGCACTT 300
DB 241 CAGGTTCCGATTAATCTTTTCAAGGGGGCCCTAAGTGGGGCCGCTTGGGCACTT 300
QY 301 GTCTTTGGGGCTCCCTGTGTGTGAGAGTGTCAAGAAATGAGAGCTTTGTGAG 360
DB 301 GTCTTTGGGGCTCAGCTGTGTGTGAGAGTGTCAAGAAATGAGAGCACTGTGAG 360
QY 361 CAAGTCCAGAGATTGATGCTGTGCTTACCTGAGACAGCTGTGCTGATCTGATCAG 420
DB 361 CAAGTCCAGAGATTGATGCTGTGCTTACCTGAGACAGCTGTGCTGATCTGATCAG 420
QY 421 AGTGGGGGCTGGGGCGGACTTCAAGCTTATAGGGGAGCGGGCCCTGAGAGACGAG 480
DB 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTTATAGGGGAGCGGGCCCTGAGAGACGAG 480
QY 481 CGCTCTCGGAGAGGGAACTGGGCACTGAGAGACAGTGTCTGACGGGGCCGTGGACT 540
DB 481 CGCTCTCGGAGAGGGAACTGGGCACTGAGAGAGACAGTGTCTGACGGGGCCGTGGACT 540
QY 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
DB 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581

RESULT 12
ABT16642
ID ABT16642 standard; DNA; 3542 BP.
XX
AC ABT16642;
XX
DT 03-APR-2003 (first entry)
XX
DE Human bcl-2 gene SEQ ID No 4.
XX
KW Anti-tumour; DNzyme; bcl-2 gene; tumour; malignant; chemotherapy;
XX radiation therapy; catalytic domain; enzyme; human; ds.
XX
OS Homo sapiens.
XX
PN W0200299090-A1.
XX
PD 12-DEC-2002.
XX
PF 07-JUN-2002; 2002W0-AU000739.
XX
PR 07-JUN-2001; 2001AU-00005527.
XX
PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;
XX
WPI; 2003-140617/13.

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XX Novel DNzyme useful for treating tumors, and for enhancing the
 PT sensitivity of malignant or virus infected cells to therapy, comprises a
 PT catalytic domain and binding domain contiguous to the catalytic domain.
 PS Disclosure; Page 44-45; 67pp; English.

XX The invention relates to a DNzyme which specifically cleaves mRNA
 CC transcribed from a member of the bcl-2 gene family. The DNzymes comprise
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of
 CC the catalytic domain, and therefore hybridise with, the two regions
 CC immediately flanking the putative residue of the cleavage site within the
 CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A
 CC pharmaceutical composition comprising a DNzyme of the invention is
 CC useful for treating tumors in a subject, and for enhancing the
 CC sensitivity of malignant or virus infected cells infected cells to
 CC therapy. The DNzymes are useful in diagnostics, therapeutics,
 CC prophylaxis, research agents and in kits. The DNzymes are also useful
 CC for increasing the susceptibility of tumour cells to anti-tumour
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide
 CC sequence represents a human bcl-2 gene of the invention

XX Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Query Match 86.5%; Score 502.6; DB 7; Length 3542;
 Best Local Similarity 91.6%; Pred. No. 2.1e-126;
 Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCGAGCTCAACCCAGACACAGCGCTTACTAGCTGACTTTGAGGCTAT 60
DB 1.77 ATGGCGACCCGAGCTTGGCCCGACACACGCGCTTGTGGAGACTTTGAGGTTAT 236
QY 61 AGCGTAGAGCAGAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGGCCAGCGCCGAC 120
DB 61 AAGCTAGAGCAGAGGGTTATGTCTGTGAGAGCTGGGCTGGGGAGGCCAGCGAGCTGAC 120
QY 121 CCGGTGACCAAGGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTCCCGCCGAC 180
DB 121 CCGGTGACCAAGGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTCCCGCCGAC 180
QY 237 AAGCTGAGGCGAGAGGGTTATGTCTGTGAGAGCTGGGCCCGGGAGGGCCAGCAGCTGAC 296
DB 237 AAGCTGAGGCGAGAGGGTTATGTCTGTGAGAGCTGGGCCCGGGAGGGCCAGCAGCTGAC 296
QY 297 CCGGTGACCAAGGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTCCCGCCGAC 356
DB 297 CCGGTGACCAAGGCATGCGGGCTGCTGAGAGAGAGTTTGAACCCGTTCCCGCCGAC 356
QY 301 GTCTTTGGGGCTCCCTGTGTGTGAGAGTGTCAAGAAATGAGAGCTTTGTGAGGGA 360
DB 301 GTCTTTGGGGCTCCCTGTGTGTGAGAGTGTCAAGAAATGAGAGCTTTGTGAGGGA 360
QY 417 CAGGTTCCGAGTAACCTTTTCAAGGGGGCCCAAGTGGGGCCGCTTGTGAGCTTCTT 476
DB 417 CAGGTTCCGAGTAACCTTTTCAAGGGGGCCCAAGTGGGGCCGCTTGTGAGCTTCTT 476
QY 477 GTCTTTGGGGCTGACGTGTGTGAGAGTGTCAAGAGAGATGAGAACCACTGTGGGA 536
DB 477 GTCTTTGGGGCTGACGTGTGTGAGAGTGTCAAGAGAGATGAGAACCACTGTGGGA 536
QY 361 CAAGTCCAGAGATTGATGCTGTGCTTACCTGAGACAGCTTTGCTACTGATCCAGAGC 420
DB 361 CAAGTCCAGAGATTGATGCTGTGCTTACCTGAGACAGCTTTGCTACTGATCCAGAGC 420
QY 537 CAAATGCAAGAGTGAATGAGGCTTACTGAGAACCGGGCTGCTGATGAGATCCAGAGC 596
DB 537 CAAATGCAAGAGTGAATGAGGCTTACTGAGAACCGGGCTGCTGATGAGATCCAGAGC 596
QY 421 AGTGGGGGCTGGGGCGGACTTCAAGCTTCTTACGGGGAGCGGGCCCTGAGAGACGAG 480
DB 421 AGTGGGGGCTGGGGCGGAGTTCAAGCTTCTTACGGGGAGCGGGCCCTGAGAGAGCGAG 480
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DB 597 AGTGGGGGCTGGGGCGGAGTTCAAGCTTCTTACGGGGAGCGGGCCCTGAGAGAGCGAG 656
QY 481 CGTCTGCGGAGAGGCAACTGGGATGATGAGAGCAGTGTGACGGGGGCGCTGTGAGACT 540
DB 481 CGTCTGCGGAGAGGCAACTGGGATGATGAGAGCAGTGTGACGGGGGCGCTGTGAGACT 540
QY 657 CGTCTGCGGAGAGGCAACTGGGATGATGAGAGCAGTGTGACGGGGGCGCTGTGAGACT 716
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QY 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 581
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DB 717 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTG 757

RESULT 13
AAT96577
ID AAT96577 standard; DNA; 583 BP.
XX

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AC AAT96577;
 XX 22-APR-1998 (first entry)
 XX Human bcl-w DNA.
 XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
 XX diagnosis; degenerative disease; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT 1..582
 FT CDS /*tag= a
 FT /product= "bcl-w"
 XX MO9735971-A1.
 XX PD 02-OCT-1997.
 XX PF 27-MAR-1997; 97WO-AU000199.
 XX PR 27-MAR-1996; 96AU-00008965.
 XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX PI Cory S, Adams JM, Gibson LM, Holmgren SP;
 XX MPI: 1997-489635/45.
 XX P-PSDB; AAM36047.
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 XX inhibit cell survival, e.g. for treatment of cancer and degenerative
 XX diseases.
 XX Claim 3; Page 48; 86pp; English.
 XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
 XX family, extracted from an adult brain library. This gene promotes cell
 XX survival, so its modulation is useful in treatment of cancer or auto-
 XX immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease,
 XX myocardial infarct, muscular degeneration, hypoxia, ischaemia, human
 XX immunodeficiency virus infection or in cell transplants. Up-regulation of
 XX the gene can also be used to modify cell lines cultured in vivo, e.g. to
 XX develop new lines, to facilitate isolation of hybridomas and to increase
 XX survival of primary explants during genetic modification. It can be used
 XX to produce recombinant Bcl-w for therapy, diagnosis, antibody production
 XX or screening of potential modulators
 XX CC
 XX CC
 XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
 SQ
 Query March 86.2%; Score 501; DB 2; Length 583;
 Best Local Similarity 91.4%; Pred. No. 3.4e-126;
 Matches 531; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1 ATGCCGACCCAGCCTCAACCCAGACACACGCGCTCTAGTGTGATTTGAGGCTAT 60
 DB 1 ATGCCGACCCAGCCTCGGCCCCAGACACACGCGCTCTGATGAGACTTTGATAGTTAT 60
 QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGACTGCGGCTTGGGAGAGGCCAGCCGCGAC 120
 DB 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGACTGCGGCTTGGGAGAGGCCAGCGTAC 120
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 QY 181 TTCTCTGACTGGCGCTCAGCTACGTCAGCCAGGCTCAGCCAGCAAGCTTAC 240
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DB 241 CAGGTTTCCGACGAATTTTCCAAAGGGGCGCTTAATGCGGCGCTTGTGCAATTTCT 300
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 QY 361 CAAGTCCAGGATTTGATGCTGAGCCTTCTGAGACACGCTGAGCTGATGATCAGAC 420
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 DB 541 GGGGCGCTGTACTGTAGGGGCGCTTTTGTCTAGCAAGT 581
 RESULT 14
 ID AAX25134
 ID AAX25134 standard; DNA; 583 BP.
 AC AAX25134;
 XX 05-JUL-1999 (first entry)
 XX Human bcl-w gene derivative.
 XX DE Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
 XX KW animal model; ss.
 XX OS Homo sapiens.
 XX PN MO9913710-A1.
 XX PD 25-MAR-1999.
 XX PF 16-SEP-1998; 98MO-AU000764.
 XX PR 16-SEP-1997; 97AU-00009228.
 XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
 XX MPI: 1999-243890/20.
 XX P-PSDB; AAY05532.
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or
 XX PT protein associated with Bcl-w.
 XX PS Disclosure; Page 36; 52pp; English.
 XX The present sequence is described as a derivative of the human bcl-w gene
 XX (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival
 XX member of the Bcl-2 family which is widely expressed and which is
 XX essential for spermatogenesis. The invention relates generally to a
 XX method of treatment and to an animal model for the identification of
 XX molecules and genetic sequences useful for inducing or reducing fertility
 XX of male animals. Methods are provided for the treatment of infertility,
 XX or for reducing fertility, by modulating spermatogenesis. An animal model
 XX carries a mutation in at least one allele of the human or murine bcl-w
 XX gene or in a gene associated with bcl-w. Such animals have disorganised
 XX seminiferous tubules and are substantially infertile, but possess no other
 XX major abnormalities as determined by histological examination. They can
 XX be used to screen for therapeutic molecules including genetic sequences
 XX capable of inducing, enhancing or otherwise facilitating spermatogenesis
 XX in animals, or which can induce infertility

XX Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 U; 0 Other;
SQ

| | | | | |
|---------------------------|--------|---------------------|-----------|-------------|
| Query Match | 86.2%; | Score 501; | DB 2; | Length 583; |
| Best Local Similarity | 91.4%; | Pred. No. 3.4e-126; | | |
| Matches 531; Conservative | 0; | Mismatches 50; | Indels 0; | Gaps 0; |

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| QY | 1 | ATGGCGACCCAGCCTCAACCCCAACACACCGCGCTCAGTGGCTGACCTTGTACGAT | 60 |
| Db | 1 | ATGGGACCCCAAGCCTCGGGCCCCCAACACACCGGGCTCTGTGTGGACACTTTGTAGTTAT | 60 |
| QY | 61 | AGCCTGAGGACAGAGGGTTATGTCTGTGAGCTGGGCTTGGGGAAAGGCCACGCCGAC | 120 |
| Db | 61 | AAGCTGAGGACAGAAAGGTTATGTCTGTGAGCTGGACCCCGGGGAGAGGCCACAGACTGAC | 120 |
| QY | 121 | CCGCTGCACCAAGCCATGCGGGCTCTGTGAGACAGATTGAAACCCGTTTCGGCCGAC | 180 |
| Db | 121 | CCGCTGCACCAAGCCATGCGGGCACTGGAGTGAATTCGAAACCCGCTTCGGCGCAC | 180 |
| QY | 181 | TTCTCTGACCTGGCCGCTCAGCTAACGACGCCACAGCCTCAGCCACAGACGCTTCA | 240 |
| Db | 181 | TTCTCTGATCTGGCGGCTCAGCTGATGTGAACCCAGCTCAGCCACAGAACGCTTCA | 240 |
| QY | 241 | CAGGTTTCCAGCAACTTTTCCAAAGGGGCCCTTAACTGGGGCGCTTGTGTGCAATCTT | 300 |
| Db | 241 | CAGGCTCCAGACAACTTTTCAAGGGGCCCCAACTGGGGCGGCTTGTAGCCTTCTT | 300 |
| QY | 301 | GTCCTTGGGGCGCCCTGTGTGCTGAGATGTTCACAAAGAAATGAGCCTTTGGTGG | 360 |
| Db | 301 | CTCTTTGGGGCTGCACTGTGTGCTAGAGTGTCCAAAGGAATGAACCACTGTGTGGA | 360 |
| QY | 361 | CAAGTCAGAGATTGATCGTGGCTACCTCGAGACAACGTCGTGATCTGAATCCAC | 420 |
| Db | 361 | CAAGTCAGAGATGATGTGGCTTACCTCGAGACGCGGCTGTGATCTGAATCCAC | 420 |
| QY | 421 | AGTGCAGGCTGCGCGGACTTCAAGACTCTATACGCGGACGCGGCCCTGTGAGACG | 480 |
| Db | 421 | AGTGGGGGCTGTGGCGGAGTTTCAAGCTCTATACGCGGAAAGCGGCCCTGTGAGAGCG | 480 |
| QY | 481 | CGTCTGCGGAGAGGCAACTGGGCATGAGTGAACAAGTGTGACGCGGGCCGTGGCACT | 540 |
| Db | 481 | CGTCTGCGGAGAGGCAACTGGGCATCAGTGAAGACAAGTGTGACGCGGGCCGTGGCACT | 540 |
| QY | 541 | GGGGGCGCTGTACTGTGAGAGGGCCCTTTTGTGTACAGATG | 581 |
| Db | 541 | GGGGGCGCTGTACTGTGAGAGGGCCCTTTTGTGTACAGATG | 581 |

RESULT 15
AAV28334
ID AAV28334 standard; cDNA; 579 BP.

AC AA V28334

DT 02-OCT-1998 (first entry)

Human bcl-*y* gene.

bs; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

OS Homo sapiens.
XY

| HH | Key | Location/Qualifiers |
|----|-----|---------------------|
| ET | CDS | 1 579 |

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/NOTE = NO RECORD GIVEN

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XX 23-FEB-1996; 96US-0012201P.
PR
RU

PA (COCE-) COCENSYS INC.

Guastella J. PI
vvy

DR WPI; 1998-446079/38
DP P-PSNB. 2AW61392

Nucleic acids and

PT recombinant protein for use in treating uncontrolled cell growth e.g. cancers.

xx
PS Claim 3: Column 15/16: 27pb: English.

The mammalian bcl-2 genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-2 falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;

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| Query Match | 85.6%; | Score 497.4; | DB 2; | Length 579; |
| Best Local Similarity | 91.2%; | Pred. No. 3.2e-125; | | |
| Matches 528; Conservative | 0; | Mismatches 51; | Indels 0; | Gaps 0 |

[illegible]

Mon Mar 29 09:44:48 2004

us-09-155-327g-8.png

Page 12

Job time : 363.378 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: March 29, 2004, 04:20:47 ; Search time 76.3686 Seconds

(without alignments)
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Title: US-09-155-327G-8
Perfect score: 581

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

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| 5 | 364.8 | 62.8 | 1098 | 4 US-09-010-147B-23 | Sequence 23, Appli |
| 6 | 364.8 | 62.7 | 1864 | 4 US-09-149-476-130 | Sequence 130, App |
| 7 | 134.6 | 23.2 | 926 | 1 US-08-081-448-5 | Sequence 6, Appli |
| 8 | 134.6 | 23.2 | 926 | 2 US-08-470-670A-6 | Sequence 1, Appli |
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| 28 | 125 | 21.5 | 5094 | 4 US-09-234-186-7 | Sequence 7, Appli |
| 29 | 125 | 21.5 | 5104 | 6 5506344-1 | Patent No. 5506344 |
| 30 | 125 | 21.5 | 6030 | 4 US-09-023-655-1015 | Sequence 1015, Ap |
| 31 | 123.4 | 21.2 | 760 | 1 US-08-405-702A-11 | Sequence 11, Appli |
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| 38 | 120.2 | 20.7 | 1303 | 4 US-09-271-014A-1 | Sequence 1, Appli |
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| 43 | 115.8 | 19.9 | 831 | 6 5459251-3 | Patent No. 5459251 |
| 44 | 115.8 | 19.9 | 831 | 6 5506344-4 | Patent No. 5506344 |
| 45 | 113.8 | 19.6 | 1384 | 4 US-08-899-367-1 | Sequence 1, Appli |

ALIGNMENTS

```
RESULT 1
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; US-08-798-897-1
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; Query Match: 93.0%; Score 540.6; DB 1; Length 579;
; Best Local Similarity: 95.9%; Pred. No. 2.1e-144;
; Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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DB 1 ATGCGAGCCAGCCTCAACCCAGACACAGCAGCTAGTGTGATTTGAGGTAT 60
QY 61 AGGCTGAGGAGGAGGATTATGTGTGAGAGCTGGGCTGGGAGAGGCCAGCCGCGAC 120

Db 61 AAGCTGAGACAGAGGGTTATGCTGTGTGAGCTGGCCCTGGGGAAGCCAGAGCCGAC 120
Qy 121 CCGCTGACCAAGCAAGCGGAGCTGTGTGAGAGCAAGTTTGAAGCCCTTTCCGCGGAC 180
Db 121 CCGCTGACCAAGCAAGCGGAGCTGTGTGAGAGCAAGTTTGAAGCCCTTTCCGCGGAC 180
Qy 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTACAC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTACAC 240
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Db 241 CAGGTTTCCAGCAAGCTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGGCAATCTTT 300
Qy 301 GTCTTTGGGGCTGCTGT 360
Db 301 GTCTTTGGGGCTGCTGT 360
Qy 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Db 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Qy 421 AGTGGCGGCTGGCGGAGCTTACAGCTCTATACGGGAGCGGCGCTTGGAGACGCA 480
Db 421 AGTGGCGGCTGGCGGAGCTTACAGCTCTATACGGGAGCGGCGCTTGGAGACGCA 480
Qy 481 CGTCTGCGGAGGAGCACTGGGATGATGAGACAGCTGTGTGTGTGTGTGTGTGTGT 540
Db 481 CGTCTGCGGAGGAGCACTGGGATGATGAGACAGCTGTGTGTGTGTGTGTGTGTGT 540
Qy 541 GGGGCGCTGTACTGTATGAGGGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Db 541 GGGGCGCTGTACTGTATGAGGGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579

RESULT 2

US-08-978-523-1

Sequence 1, Application US/08978523

Patent No. 5883229

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483, 0140002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-978-523-1

Query Match 93.0%; Score 540.6; DB 2; Length 579;
Best Local Similarity 95.9%; Pred. No. 2.1e-144;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ATGCCAGCCCAAGCCCTCAACCCAGACACAGCGCTCTAGTGTGATTTGATAGGCTAT 60
Db 1 ATGCCAGCCCAAGCCCTCAACCCAGACACAGCGGCTCTAGTGTGATTTGATAGGCTAT 60
Qy 61 AGCTGAGGACAGAGGTTATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 AGCTGAGGACAGAGGTTATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy 121 CCGCTGACCAAGCAAGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 121 CCGCTGACCAAGCAAGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Qy 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTACAC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAACCCAGGCTCAGCCGCAAGCTTACAC 240
Qy 241 CAGGTTTCCAGCAAGCTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGGCAATCTTT 300
Db 241 CAGGTTTCCAGCAAGCTTTTCCAAAGGGGCGCTTACTGAGGCGCTTGTGGCAATCTTT 300
Qy 301 GTCTTTGGGGCTGCTGT 360
Db 301 GTCTTTGGGGCTGCTGT 360
Qy 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Db 361 CAAGTCCAGAGATTGATCGTGGCTACCTGGAGACAGTGTGGCTGATGATCCAGC 420
Qy 421 AGTGGCGGCTGGCGGAGCTTACAGCTCTATACGGGAGCGGCGCTTGGAGACGCA 480
Db 421 AGTGGCGGCTGGCGGAGCTTACAGCTCTATACGGGAGCGGCGCTTGGAGACGCA 480
Qy 481 CGTCTGCGGAGGAGCACTGGGATGATGAGACAGCTGTGTGTGTGTGTGTGTGTGT 540
Db 481 CGTCTGCGGAGGAGCACTGGGATGATGAGACAGCTGTGTGTGTGTGTGTGTGTGT 540
Qy 541 GGGGCGCTGTACTGTATGAGGGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
Db 541 GGGGCGCTGTACTGTATGAGGGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579

RESULT 3

US-08-798-897-2

Sequence 2, Application US/08798897

Patent No. 5789201

GENERAL INFORMATION:

APPLICANT: Guastella, John

TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/798,897
 FILING DATE: February 11, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1483.0140001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 579 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-08-798-897-2

Query Match 85.6%; Score 497.4; DB 1; Length 579;
 Best Local Similarity 91.2%; Pred. No. 4e-132;
 Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGCCGACCCAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
QY 61 AGCGTGAAGCAGAGGTTATGTCGTGAGCTGGGCTGGGAGAGCCGACCGGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGCTGGGCTGGGAGAGCCGACGAGTGAC 120
QY 121 CCGCTGACCAACCCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTCCGCGCAC 180
DB 121 CCACTGACCAACCCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCCCTGACGTAACAGTGAACCCGAGGCTCAAGCCAGAGGCTTAC 240
DB 181 TTCTCTGATCTGGCGCTGACGTCAGTCAGTGAACCCGAGGCTCAAGCCAGAGGCTTAC 240
QY 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGCTTTGAGCATTTCTT 300
DB 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGCTTTGAGCATTTCTT 300
QY 301 GTCTTTGGGGCTGCTGCTGAGTGAAGTGAACAAAGAAATGAGAGCTTTGAGGGA 360
DB 301 GTCTTTGGGGCTGCTGCTGAGTGAAGTGAACAAAGAAATGAGAGCTTTGAGGGA 360
QY 361 CAACTGACAGATGATGCTGAGCTTACCTGAGAGACGTCCTGAGCTGACTGATCCAC 420
DB 361 CAACTGACAGATGATGCTGAGCTTACCTGAGAGACGTCCTGAGCTGACTGATCCAC 420
QY 421 AAGTGGGCGCTGGGCGCTGACGTAAGTGAAGTGAACCCGAGGCTCAAGCCAGAGG 480
DB 421 AAGTGGGCGCTGGGCGCTGACGTAAGTGAAGTGAACCCGAGGCTCAAGCCAGAGG 480
QY 481 CGTCTGCGGAGAGGAGCACTGGGCGATGAGAGCAAGTGTGACGCGGCGCTTGAC 540
DB 481 CGTCTGCGGAGAGGAGCACTGGGCGATGAGAGCAAGTGTGACGCGGCGCTTGAC 540
QY 541 GGGGCGCTGATGATCTGTAGGGGCTTTTGTGCTAGCAAG 579
DB 541 GGGGCGCTGATGATCTGTAGGGGCTTTTGTGCTAGCAAG 579

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RESULT 4
 US-08-978-523-2
 Sequence 2, Application US/08978523
 Patent No. 5883229
 GENERAL INFORMATION:
 APPLICANT: Gustella, John
 TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,523
 FILING DATE: herewith
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/798,897
 FILING DATE: February 11, 1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1483.0140002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 579 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 US-08-978-523-2

Query Match 85.6%; Score 497.4; DB 2; Length 579;
 Best Local Similarity 91.2%; Pred. No. 4e-132;
 Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 1 ATGCCGACCCAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
DB 1 ATGCCGACCCAGCTCAACCCGACACACGCGCTCTAGTGGCTGACTTTGAGGCTAT 60
QY 61 AGCGTGAAGCAGAGGTTATGTCGTGAGCTGGGCTGGGAGAGCCGACCGGAC 120
DB 61 AAGCTGAGGAGAGAGGTTATGTCGTGAGCTGGGCTGGGAGAGCCGACGAGTGAC 120
QY 121 CCGCTGACCAACCCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTCCGCGCAC 180
DB 121 CCACTGACCAACCCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTCCGCGCAC 180
QY 181 TTCTCTGACCTGGCCCTGACGTAACAGTGAACCCGAGGCTCAAGCCAGAGGCTTAC 240
DB 181 TTCTCTGATCTGGCGCTGACGTCAGTCAGTGAACCCGAGGCTCAAGCCAGAGGCTTAC 240
QY 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGCTTTGAGCATTTCTT 300
DB 241 CAGGTTCCGACCACTTTTCAAGGGGCGCTTAAGTGGGCGCTTTGAGCATTTCTT 300
QY 301 GTCTTTGGGGCTGCTGCTGAGTGAAGTGAACAAAGAAATGAGAGCTTTGAGGGA 360
DB 301 GTCTTTGGGGCTGCTGCTGAGTGAAGTGAACAAAGAAATGAGAGCTTTGAGGGA 360
QY 361 CAACTGACAGATGATGCTGAGCTTACCTGAGAGACGTCCTGAGCTGACTGATCCAC 420
DB 361 CAACTGACAGATGATGCTGAGCTTACCTGAGAGACGTCCTGAGCTGACTGATCCAC 420
QY 421 AAGTGGGCGCTGGGCGCTGACGTAAGTGAAGTGAACCCGAGGCTCAAGCCAGAGG 480
DB 421 AAGTGGGCGCTGGGCGCTGACGTAAGTGAAGTGAACCCGAGGCTCAAGCCAGAGG 480

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QY 481 CGTCTGCGGAGGCGCACTGGGCATGAGTACACAGTGTGTACCGGGGCGCTGGCACTG 540
Db 481 CGTCTGCGGAGGCGGAGCACTGGGCATGAGTACAGAGTGTGTACCGGGGCGCTGGCACTG 540
QY 541 GGGGCGCTGTACTGTAGTGGGGCGCTTTTGTCTAGCAAG 579
Db 541 GGGGCGCTGTACTGTAGTGGGGCGCTTTTGTCTAGCAAG 579

RESULT 5

US-09-010-147B-23
Sequence 23, Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010.147B
FILING DATE: 12-NO. 6653445-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034.205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034.204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-010-147B-23

Query Match 62.8% Score 364.8; DB 4; Length 1098;
Best Local Similarity 90.3%; Pred. No 2.6e-94;
Matches 390; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGCCGACCCGAGCTCAACCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGCCGACCCGAGCTCGGCCAGACACAGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCGCTGGGAAAGCCAGCCGCGGAC 120
Db 61 AAGCTGAGGCAAGAGGTTATGTCTGTGAGAGCTGGGCGCCGCGGAGGAGCCAGCGCTGAC 120
QY 121 CCGCTGCACCAAGGCATGCGGCTGCTGGAGACAGATTGTAGACCCGTTTCCGCGGACG 180

Db 121 CCGCTGCACCAAGGCATGCGGCTGCTGGAGACAGATTGTAGACCCGTTTCCGCGGACG 180
QY 181 TTCTGTGACCTGCGGCTGACGTACACGTGACGCCAGGCTGAGCCAGCAAGCTTCACG 240
Db 181 TTCTGTGACCTGCGGCTGACGTGACGTGACGCCAGGCTGAGCCAGCAAGCTTCACG 240
QY 241 CAGGTTCCGAGAACTTTTCCAGAGGCGCTTAAGTCTGGGCGCTGTGGCATTTCTT 300
Db 241 CAGGTTCCGAGAACTTTTCCAGAGGCGCTTAAGTCTGGGCGCTGTGGCATTTCTT 300
QY 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
Db 301 GTCTTTGGGGGCTGCGCTGTGTGCTGAGAGTGTCAACAAGAAATGAGACCTTTGGTGGGA 360
QY 361 CAGTCCAGAGATTGATGCTGCTGAGCTTACCTGAGACACGCTTGGCTGATCCACAGC 420
Db 361 CAGTCCAGAGATTGATGCTGCTGAGCTTACCTGAGACACGCGGCTGGCTGATCCACAGC 420
QY 421 AGTGGCGGCTGG 432
Db 421 AGTGGCGGCTGG 432

RESULT 6

US-09-149-476-130
Sequence 130, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149.476
FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040.162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038.621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040.163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047.600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047.584

[illegible]

EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057,669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049,610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997-10-02

Query Match 62.7%; Score 364.4; DB 4; Length 1864;
 Best Local Similarity 90.0%; Pred. No. 4,1e-94;
 Matches 389; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

1 ATGCCAGCCCAAGCTTCAACCCAGACACACGCGCTAGTGGTGACTTTGAGGCTAT 60
 11 ATGGGACCCCAAGCTTCCGCCCCAGACACACGCGCTGATGGCAGACTTTGATGTTAT 70
 61 AGGCTGAGGCAAGAGGTTATGCTGTGTGAGCTGGGCTTGGGAAAGCCCGCCGAC 120
 71 AAGCTGAGGCAAGAGGTTATGCTGTGTGAGCTGGGCTTGGGAAAGCCCGCCGAC 130
 121 CCGCTGACCAAGCCATCGGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGGAC 180
 131 CCGCTGACCAAGCCATCGGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGGAC 190
 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTAC 240
 191 TTCTCTGATCTGGCCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTAC 250
 241 CAGGTTTCCAGGAATTTTCCAGAGGGGCTTAACTGGGGCGCTTTGTGGCAATCTTT 300
 251 CAGGTTTCCAGGAATTTTCCAGAGGGGCTTAACTGGGGCGCTTTGTGGCAATCTTT 310
 301 GTCTTTGGGGCTGCTGCTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGT 360
 311 GTCTTTGGGGCTGCTGCTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGT 370
 361 CAGGTTTCCAGGAATTTTCCAGAGGGGCTTAACTGGGGCGCTTTGTGGCAATCTTT 420
 371 CAGGTTTCCAGGAATTTTCCAGAGGGGCTTAACTGGGGCGCTTTGTGGCAATCTTT 430
 421 AGTGGGGCTGG 432
 431 AGTGGGGCTGG 442

RESULT 7

US-08-081-448-5
 Sequence 5, Application US/08081448
 Patent No. 5646008
 GENERAL INFORMATION:
 APPLICANT: Thompson, Craig B.
 APPLICANT: Boise, Lawrence H.
 TITLE OF INVENTION: Vertebrate Apoptosis Gene:
 TITLE OF INVENTION: Compositions and Methods
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5646008th Clark Street, Suite 800
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,448
 FILING DATE: 19930622
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5646008thrup, Thomas E.

REGISTRATION NUMBER: 33,268
 REFERENCE/DOCKET NUMBER: ARCD090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-744-0090
 TELEFAX: 312-755-4489
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 926 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 135..836
 US-08-081-448-5

Query Match 23.2%; Score 134.6; DB 1; Length 926;
 Best Local Similarity 58.3%; Pred. No. 7,1e-29;
 Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

128 ACCAAGCATGCGGGCTGCTGAGAGCAGATTGAGACCCGTTTCCGCGCACTTCTCTG 187
 394 AGCAGAGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
 188 ACCTGGCCGCTCAGCTACAGTGAAGCCAGGCTCAGCCAGCAAGCTTCAACCAAGTTT 247
 454 ACTGACATCCAGCTCCATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
 248 CCGACCAATTTTCCAGAGGGGCTTAACTGGGGCGCTTTGTGGCAATCTTTGCTTTG 307
 514 TGAATGACCTTCCGAGATGGAGTAACTGGGGTGAATGGAGCTTTTCTCTTCC 573
 308 GGGCTGCTGCTGTGTGTGAGAGTGTCAACAAAGAAATGAGACCTTTGGTGGCAAGTCC 367
 574 GCGGGGCACTGTGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 633
 368 AGGATTGAGAGTGGGCTGCTGAGAGCAGCTGTGGCTGAGTTCAGTTCACAGCACTGGCG 427
 634 CAGCTTGAATGCTCACTTCTGAATGACCACTTGAAGCTTGAATTCAGAGAAAGCGCG 693
 428 GCTGGCGGACTTCAAGCTCTTATACGGGAGCGGGCCCTGAGAGCAGCAGCGGCTTGC 487
 694 GCTGGGATCTTTTGTGGAATCTTAATGGGAACAATGAGCAGACCCGAGAGCGGAGGCG 753
 488 GGGAGGCAACTGGGATGAGTGAACACAGTGTGTGAGCGGGCGG 532
 754 AGGAACGTTCAACCGCTGTTCTGAGCGGAGTATGTGGCCG 798

RESULT 8

US-08-470-670A-6
 Sequence 6, Application US/08470670A
 Patent No. 5834309
 Patent No. 5834309 5710045
 GENERAL INFORMATION:
 APPLICANT: Thompson, Craig B.
 APPLICANT: Boise, Lawrence H.
 TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ABCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-5000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-470-670A-6

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Query Match      23.2%; Score 134.6; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 128 ACCAAGCCATGCGGGGCTGTGAGAGAGAGTTGAGACCCGTTCCGCGCACCTTCTGTG 187
DB 394 AGCAAGCGCTGAGGAGGAGGAGGAGAGTTGAACTGGGGTACCGGCGGGCATTCAGTG 453
QY 188 ACTGCGCCCTCAGCTACACGTCGACCCCGGCTCAGCCCGAGAAAGCTTCACCCAGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCACCCCGAGGAGAGCATATCAGAGCTTTGAAACAGGTAG 513
QY 248 CCGAGCACTTTCCAAAGGGGGCCCTTAAGTGGGGCGGCTTGTGATTTCTTGTCTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTGCATTGTGCTTTTCTCTTCG 573
QY 308 GGGTGCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGACAAAGTCC 367
DB 574 GCGGGGCACTGTGCGGTGAGAAAGCGTAGACAGAGATGAGGTATTTGGTAGTCGAGTGC 633
QY 368 AGGATTGATCGTGGCTTACTGTGAGAGACGCTTGGCTGATGATCCACAGCACTGGCG 427
DB 634 CAGCTTGATGGCCACTTACTGATGACCACTTAAGGCTTGGATCCAGAGAAAGGCG 693
QY 428 GCTGGGGCGACTTCACAGCTCTATACGGGGAGAGGGGCGCTGAGAGACGACGGCGTTCG 487
DB 694 GCTGGGATTACTTTTGTGAACTCTATGGGAACATGCAAGCCAGAGCGGAAAGGCGC 753
QY 488 GGGAGGGCACTGGGATGAGAGACAGTGTGACGGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGTTCTGAGGGGATGATGTGGCG 798

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RESULT 9
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

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; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD)
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
; US-08-481-739-1

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Query Match      23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7.1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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QY 128 ACCAAGCCATGCGGGGCTGTGAGAGAGTTGAGACCCGTTCCGCGCACCTTCTGTG 187
DB 394 AGCAAGCGCTGAGGAGGAGGAGGAGAGTTGAACTGGGGTACCGGCGGGCATTCAGTG 453
QY 188 ACTGCGCCCTCAGCTACACGTCGACCCCGGCTCAGCCCGAGAAAGCTTCACCCAGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCACCCCGAGGAGAGCATATCAGAGCTTTGAAACAGGTAG 513
QY 248 CCGAGCACTTTCCAAAGGGGGCCCTTAAGTGGGGCGGCTTGTGATTTCTTGTCTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTGCATTGTGCGCTTTTCTCTTCG 573
QY 308 GGGTGCCTGTGTGTGAGAGTGTCAACAAAGAAATGAGGCTTTGTGGGACAAAGTCC 367
DB 574 GCGGGGCACTGTGCGGTGAGAAAGCGTAGACAGAGATGAGTATTTGGTAGTCGAGTGC 633
QY 368 AGGATTGATCGTGGCTTACTGTGAGAGACGCTTGGCTGATGATCCACAGCACTGGCG 427
DB 634 CAGCTTGATGGCCACTTACTGATGACCACTTAAGGCTTGGATCCAGAGAAAGGCG 693
QY 428 GCTGGGGCGACTTCACAGCTCTATACGGGGAGAGGGGCGCTGAGAGACGACGGCGTTCG 487
DB 694 GCTGGGATTACTTTTGTGAACTCTATGGGAACATGCAAGCCAGAGCGGAAAGGCGC 753
QY 488 GGGAGGGCACTGGGATGAGAGACAGTGTGACGGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGTTCTGAGGGGATGATGTGGCG 798

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RESULT 10
US-09-167-921-1
; Sequence 1, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Montia, Brett P.
; APPLICANT: Nickoloff, Brian J.

```

APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTTCGCCGCACTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGCATTCAATG 453
QY 188 ACCGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCACAGCGTTCAACCCAGATT 247
DB 454 ACCTGACATCCAGCTCAACATCACCCAGGAGACGATCAAGCTTGAACAGATG 513
QY 248 CCGAGCACTTTCCAAAGGGGCCCTTAAGTGGGCCCTTGTGGCAATCTTTGCTTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTCCGATTTGCTTTTCCTTCG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGTGCACAAAGAAATGAGACCTTTGGTGGACAGTCC 367
DB 574 GCGGGGCACTGTGGGTGGAAGCGTAGCAAGAGATGACAGTATTGGTAGTGAGTGC 633
QY 368 AGAATGATGCTGGGCTTAACTGAGACAGCTCTGGCTGATGATCAAGCAGTGGCG 427
DB 634 CAGCTTGATGCGCCACTTAAGCTGATGACCACTTAAGCTTGAATCCAGGAGAACGG 693
QY 428 GCTGGGGGAGCTTCAAGCTTAAACGGGGAGCGGGGCCCTGAGAGACGCAAGCGCTGC 487
DB 694 GCTGGGATATCTTTGTGGAATCTTATGGGAACATGACGACCGCGAAGGCTGAAGG 753
QY 488 GCGAGGGCACTGGGCGATGAGTGAACAGTGTGAGCGGGGGCG 532
DB 754 AGAAGCGTTCAACCGCTGTCTTCCGAGCGGCAATGATGCTGTGGCG 798

RESULT 11
US-09-277-020-39
Sequence 39, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-020-39

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTTCGCCGCACTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGCATTCAATG 453
QY 188 ACCGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCACAGCGTTCAACCCAGATT 247
DB 454 ACCTGACATCCAGCTCAACATCACCCAGGAGACGATCAAGCTTGAACAGATG 513
QY 248 CCGAGCACTTTCCAAAGGGGCCCTTAAGTGGGCCCTTGTGGCAATCTTTGCTTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGGGGTCCGATTTGTGCTTTTCCTTCG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGTGCACAAAGAAATGAGACCTTTGGTGGGACAAATCC 367
DB 574 GCGGGGCACTGTGCTGGAAGCGTAGACAAAGAGATCAGATTTGTGATGCGATGC 633
QY 368 AGAATGATGCTGGGCTTAACTGAGACAGCTGTGCTGATGATCAAGCAGAGTGGCG 427
DB 634 CAGCTTGATGCGCCACTTAAGCTGAAATGACCACTTGAAGCTTGAATCAAGAGAACGG 693
QY 428 GCTGGGGGAGCTTCAAGCTTAAACGGGGAGCGGGGCCCTGAGAGACGCAAGCGCTGC 487
DB 694 GCTGGGATATCTTTGTGGAATCTTATGGGAACATGACAGACGCGAAGCGGAAAGGCG 753
QY 488 GCGAGGGCACTGGGCGATGAGTGAACAGTGTGAGCGGGGGCG 532
DB 754 AGAAGCGTTCAACCGCTGTCTTCCGAGCGGCAATGATGCTGTGGCG 798

RESULT 12
US-09-323-743-1
Sequence 1, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1

Query Match 23.2%; Score 134.6; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCATGCGGGCTGCTGAGACGAGTTGAGACCCGTTTCGCCGCACTTCTCTG 187
DB 394 AGCAAGCGCTGAGGGAGGCGAGCGCGAGTTTGAATGCGGTACCGGCGGCATTCAATG 453

QY 188 ACCTGCGCGCTCACTACAGTGACCCGAGCTCAAGCCGAGCAAGCTTACCCAGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCAACCCGAGGACAGCATATCAGAGCTTTGAACAGTAG 513
QY 248 CCGAGCAATTTTCCAAAGGGGGGCCCTTAATGGGGGCCGCTTTGTGATCTTTGTCTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGAGGTCGCAATTTGAGCTTTTCTCTTCG 573
QY 308 GGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGTGGGACAAGTCC 367
DB 574 GCGGGGCACTGTGCTGCGGAAAGGTAGAAAGAGATGAGGTATTGTGAGTCCGATCG 633
QY 368 AGGATTGATCGTGGCTTACCTGAGACACGCTGCTGATCTGATTCACAGCACTGGCG 427
DB 634 CAGCTTGATGGCACTTACCTGAATGACCACTAGAGCTTGTATTCAGAGAACGCG 693
QY 428 GCTGGGCGGACTTACAGCTTATACGGGGACGGGGCCCTGAGAGACGACGCGCTTGC 487
DB 694 GCTGGGATCTTTTGTGAACTCTATGGGACAAATGACAGACCCGAGAGCCGAAAGGCGC 753
QY 488 GGGAGGGCAACTGGGATGATGAGACAGTGTGACGGGGGCGG 532
DB 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGCAATGCTGTGCGG 798

RESULT 13
US-08-461-511A-6
Sequence 6, Application US/08461511A
Patent No. 6303331

GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.B.
Boise, Lawrence H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
AND METHODS

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A

FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN

ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 135..836

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6

Query Match 23.2%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGTGAGAGAGATTGAGACCCGTTTCCGCGCACCTTCTTG 187
DB 394 AGCAAGCGCTGAGGAGAGGAGCGAGGAGTTTAACTGGGGTACCGGGCGGATTCAGTG 453
QY 188 ACCTGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTACCCAGTTT 247
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QY 368 AGGATTGATCGTGGCTTACCTGAGACACGCTGCTGATCTGATTCACAGCACTGGCG 427
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DB 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGCAATGCTGTGCGG 798

RESULT 14
US-09-271-014A-5
Sequence 5, Application US/09271014A
Patent No. 6395510

GENERAL INFORMATION:
APPLICANT: THOMPSON, CRAIG B.
BOISE, LAWRENCE H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:316

CURRENT APPLICATION NUMBER: US/09/271,014A
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 5
LENGTH: 926

TYPE: DNA
ORGANISM: Human

FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)

US-09-271-014A-5

Query Match 23.2%; Score 134.6; DB 4; Length 926;
Best Local Similarity 58.3%; Pred. No. 7,1e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 128 ACCAAGCCATGCGGGCTGTGAGAGAGATTGAGACCCGTTTCCGCGCACCTTCTTG 187
DB 394 AGCAAGCGCTGAGGAGAGGAGCGAGGAGTTTGAATGGGGTACCGGGCGGATTCAGTG 453
QY 188 ACCTGCGCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTACCCAGTTT 247
DB 454 ACCTGACATCCAGCTCCACATCAACCCAGGAGCAGATATCAGAGCTTTGAACAGTAG 513
QY 248 CCGAGCAATTTTCCAAAGGGGGGCCCTTAATGGGGGCCGCTTTGTGATCTTTGTCTTG 307
DB 514 TGAATGAATCTTCCGGGATGGGGTAACTGAGGTCGCAATTTGAGCTTTTCTCTTCG 573
QY 308 GGGCTGCGCTGTGTGCTGAGAGTGTCAAGAAATGAGAGCTTTGTGTGGGACAAGTCC 367
DB 574 GCGGGGCACTGTGCTGCGGAAAGGTAGAAAGAGATGAGGTATTGTGAGTCCGATCG 633
QY 368 AGGATTGATCGTGGCTTACCTGAGACACGCTGCTGATCTGATTCACAGCACTGGCG 427

Db 634 CAGTTTGATGGCACTTACCTGATGATGACCACTAGAGCTTGTGATCCAGAGACGGCG 693
QY 428 GCTGGGCGGACTTCACAGCTCTATACGGGAGACGGGCGCTTGAGAGACGAGCGCTTCG 487
Db 694 GCTGGGATACCTTTGTGGAATCTATGGGAACATGACGAGCGGAGAGCGGAAAGGCGC 753
QY 488 GGGAGGCGCACTGGGACATGAGTGAAGCACTGGTGAACGGGGCGG 532
Db 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGCACTGACTGTGCGG 798

RESULT 15

US-09-023-655-1430
; Sequence 1430, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0595
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1430:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g510900
; US-09-023-655-1430

Query Match

Best Local Similarity 23.2%; Score 134.6; DB 4; Length 926;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCGCTGCTGGAAGACGATTGAGACCCGTTCCGCCGACCTTCTCTG 187
Db 394 AGCAAGCGGCTGAGGAGGAGCGACGAGTTTGAATGCGGATCCGGCGGCAATTCACTG 453
QY 188 ACCTGGCGCTCAGCTACAGTGAACCCAGGCTCAGCCAGCAAGCTTCAACCAGGTTT 247
Db 454 ACCTGACATCCAGCTCCACATCAACCCAGGAGACAGCATATCAGAGCTTTGAACAGTAG 513

QY 248 CCGAGAACTTTCCAAAGGGGCGCCCTAATGAGGCGCTCTTGCGCATCTTGTCTTTG 307
Db 514 TGAATGAACCTTCCGGGATGCGGTAAACTGCGGCTCCATGTGCGCTTTTCTCCTTG 573
QY 308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGAGACCTTTGTGGACAACTCC 367
Db 574 GCGGGGCACTGTGCTGGAAGCGTAGAACAGAGATGCAAGATTTGTAGTGAATG 633
QY 368 AGAATTGATGATGCGCTACCTGAGACACGCTGTGCTGACTGATCCACAGCAGTGGCG 427
Db 634 CAGCTTGATGCGCACTTACCTGATGACCACTAGACCTTGGATCCAGAGACGCG 693
QY 428 GCTGGGCGGACTTCACAGCTCTATACGGGAGACGGGCGCTGAGAGACGACGCGGTGCG 487
Db 694 GCTGGGATACCTTTGTGGAATCTATGGGAACATGACGAGCGGAGAGCGGAAAGGCGC 753
QY 488 GGGAGGCGCACTGGGACATGAGTGAAGCAAGTGTGACGGGGCGG 532
Db 754 AGGAACGCTTCAACCGCTGCTTCTGACGGGCACTGACTGTGCGG 798

Search completed: March 29, 2004, 07:30:35
Job time : 78.3686 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein-- protein search, using sw model

Run on: March 25, 2004, 15:35:20 ; Search time 36 Seconds

(without alignments)
1691.528 Million cell updates/sec

Title: US-09-155-327g-9

Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADPVGY.....LTGAVALGALYVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1005 | 99.6 | 219 | 11 | Q7TS60 |
| 3 | 965 | 95.6 | 193 | 11 | Q8CGJ4 |
| 4 | 770 | 76.3 | 178 | 11 | Q8CYW5 |
| 5 | 770 | 76.3 | 178 | 11 | Q8CFR2 |
| 6 | 439.5 | 43.6 | 233 | 6 | Q9MYW4 |
| 7 | 435.5 | 43.2 | 233 | 11 | Q35844 |
| 8 | 433.5 | 42.9 | 233 | 6 | Q8SQ42 |
| 9 | 431.5 | 42.8 | 233 | 6 | Q8H1A2 |
| 10 | 428.5 | 42.5 | 233 | 6 | Q9MZS7 |
| 11 | 412 | 40.8 | 236 | 11 | Q8BQR4 |
| 12 | 412 | 40.8 | 236 | 11 | Q7TSN8 |
| 13 | 405 | 40.2 | 79 | 11 | Q7TS61 |
| 14 | 401 | 39.7 | 180 | 6 | Q9BDJ5 |
| 15 | 401 | 39.7 | 217 | 11 | Q9JN55 |
| 16 | 400 | 39.6 | 238 | 13 | Q90Z98 |

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| 17 | 398.5 | 39.5 | 180 | 6 | Q9BDX7 | Q9bdx7 bos taurus |
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| 19 | 395.5 | 39.2 | 235 | 6 | Q81008 | Q81008 felis silve |
| 20 | 380.5 | 37.7 | 284 | 11 | Q7RS62 | Q7rs62 rattus norv |
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| 22 | 374.5 | 37.1 | 235 | 11 | Q35843 | Q35843 mus musculu |
| 23 | 372.5 | 36.9 | 188 | 4 | Q9H1K6 | Q9h1k6 homo sapien |
| 24 | 371 | 36.8 | 204 | 13 | Q9QZH2 | Q9qzh2 xenopus lae |
| 25 | 365.5 | 36.2 | 153 | 6 | Q7YRB6 | Q7yrb6 canis fami |
| 26 | 353 | 35.0 | 185 | 6 | Q8WJ81 | Q8wj81 bos taurus |
| 27 | 347 | 34.4 | 219 | 11 | Q99N35 | Q99n35 mus musculu |
| 28 | 342.5 | 33.9 | 159 | 11 | Q8C5P0 | Q8c5p0 mus musculu |
| 29 | 296 | 29.3 | 89 | 13 | Q8WUJ1 | Q8wu11 gallus gall |
| 30 | 187 | 18.5 | 209 | 11 | Q9JKE9 | Q9jke9 rattus norv |
| 31 | 185 | 18.3 | 170 | 11 | Q9WU15 | Q9wu15 rattus norv |
| 32 | 182 | 18.0 | 209 | 11 | Q8C264 | Q8c264 mus musculu |
| 33 | 174.5 | 17.3 | 182 | 13 | Q919N4 | Q919n4 brachydario |
| 34 | 172.5 | 17.1 | 221 | 13 | Q98U13 | Q98u13 xenopus lae |
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| 36 | 168.5 | 16.7 | 125 | 4 | Q9H1R5 | Q9h1r5 homo sapien |
| 37 | 163 | 16.2 | 235 | 5 | Q967D2 | Q967d2 geodia cydo |
| 38 | 162 | 16.1 | 58 | 11 | Q9R1B3 | Q9r1b3 rattus norv |
| 39 | 157.5 | 15.6 | 153 | 6 | Q9MZS6 | Q9mzs6 ovis aries |
| 40 | 156.5 | 15.5 | 173 | 11 | Q8KJ2 | Q8kj2 mus musculu |
| 41 | 154 | 15.3 | 173 | 11 | Q8W249 | Q8w249 homo sapien |
| 42 | 154 | 15.3 | 173 | 11 | Q9JKL3 | Q9jkl3 rattus norv |
| 43 | 151 | 15.0 | 67 | 6 | Q8MTB3 | Q8mtb3 cervus elap |
| 44 | 149 | 14.8 | 192 | 6 | Q8SQ43 | Q8sq43 felis silve |
| 45 | 148.5 | 14.7 | 218 | 5 | Q9N754 | Q9n754 suberites d |

ALIGNMENTS

RESULT 1

088996 ID AC 088996 PRELIMINARY; PRT; 193 AA.

01-NOV-1998 (TREMBLrel. 08, Created)

01-NOV-1998 (TREMBLrel. 08, Last sequence update)

01-OCT-2003 (TREMBLrel. 25, Last annotation update)

Bcl-w.

BCL-W.

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

[1]

SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley; TISSUE=Brain;

MEDLINE=99292146; PubMed=1036024;

Hammer S., Skogiosa Y., Lindholm D.;

"Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";

Neuroscience 91:673-684 (1999).

[2]

SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley;

MEDLINE=22672518; PubMed=12787069;

Ich T., Ich A., Pleasure D.;

"Bcl-2-related protein family gene expression during oligodendroglial differentiation.";

J. Neurochem. 85:1500-1512(2003).

EMBL: AF096291; AAC64200.1; -

EMBL: AY185098; AAC64468.1; -

HSCP; Q07817; IMAZ.

GO: GO:0016329; F:Apoptosis; regulator activity; IEA.

GO: GO:0006915; P:Apoptosis; IEA.

InterPro: IPR000712; Bcl2 BH.

InterPro: IPR003093; Bcl2 BH.

InterPro: IPR002475; BCL2_family.

Pfam: PF00452; Bcl2; 1.

Pfam: PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PSS01080; BH1; 1.
DR PROSITE; PSS01258; BH2; 1.
DR PROSITE; PSS01260; BH4_1; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 193;
Best Local Similarity 99.5%; Pred. No. 3.9e-81;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 120
DB 61 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 120
QY 121 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 2
QTS60 PRELIMINARY; PRT; 219 AA.
AC QTS60;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BCL-WBL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=2672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
differentiation";
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AY185100; AA064470.1; -
SQ SEQUENCE 219 AA; 23720 MW; 30B36041BC1DC66F CRC64;

Query Match 99.6%; Score 1005; DB 11; Length 219;
Best Local Similarity 99.5%; Pred. No. 4.6e-81;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 2 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 86
QY 61 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 120
DB 87 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 146
QY 121 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 180
DB 147 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 206
QY 181 GALVTVGAFPAK 193
DB 207 GALVTVGAFPAK 219

RESULT 3
Q8CGI4 PRELIMINARY; PRT; 193 AA.
AC Q8CGI4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcl2-like protein 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Skin;

RA Su H.-Y.;
RT "Extraction from neonatal mouse skin after IGF-1 stimulation";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170344; AA01377.1; -
DR WGD; NGI:108052; Bcl2L2.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_FAMILY.
DR Pfam; PF00452; BCL-2; 1.
DR Pfam; PF0180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PSS01080; BH1; 1.
DR PROSITE; PSS01258; BH2; 1.
SQ SEQUENCE 193 AA; 20950 MW; 258AC181816DFA0 CRC64;

Query Match 95.6%; Score 965; DB 11; Length 193;
Best Local Similarity 96.4%; Pred. No. 1.4e-77;
Matches 186; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
DB 1 MATPASTPPTRALVADFGVYKLRQKGYVCGAGPGEPPADPLHQARRAAGDEFETFRRT 60
QY 61 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 120
DB 61 FSDLAALHTVTPGSAQORFTQVSDLFQGGPNMGRIVAFVFGAALCAESVKNKEPVLV 120
QY 121 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 180
DB 121 QVQDMWVAVLETRLDLADWVHSSGGMAEFTLYGDPGALBEARRLRGNWASVRTLGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 4
Q9CYW5 PRELIMINARY; PRT; 178 AA.
AC Q9CYW5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl2-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adachi T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishii K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asbunier M., Batalov S., Cavaant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Balarelli R., Barsh G.,
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., McInnes P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlschki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL EMBL; AK013244; BAB28740.1; -.
DR HSSP; Q07817; 1MA2.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 76.3%; Score 770; DB 11; Length 178;
Best Local Similarity 96.7%; Pred. No. 2,3e-60;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFEFRFRT 60
DB 1 MATPASTPTDTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFEFRFRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDDELFOGCPNMGRLVAFVFGALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDDELFOGCPNMGRLVAFVFGALCAESVKNKEPPLVG 120
QY 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150
DB 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150
Db 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150

RESULT 5
Q8CFR2 PRELIMINARY; PRT; 178 AA.
AC Q8CFR2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DB Bcl2-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;

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RL Submitted (NCV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040369; AAH40369.1; -.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match 76.3%; Score 770; DB 11; Length 178;
Best Local Similarity 96.7%; Pred. No. 2,3e-60;
Matches 145; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFEFRFRT 60
DB 1 MATPASTPTDTRALVADFVGYKLRQKGYVCGAGPGEPPADPLHQARRAGDEFEFRFRT 60
QY 61 FSDLAQLHTVTPGSAQQRFTQVSDDELFOGCPNMGRLVAFVFGALCAESVKNKEPPLVG 120
DB 61 FSDLAQLHTVTPGSAQQRFTQVSDDELFOGCPNMGRLVAFVFGALCAESVKNKEPPLVG 120
QY 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150
DB 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150
Db 121 QVODMNVAYLETRLDWIMHSSGGWAEFTAL 150

RESULT 6
Q9MYT4 PRELIMINARY; PRT; 233 AA.
AC Q9MYT4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DB Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC knott J.C., Robertson L., James E.R.;
RT "Rabbit Bcl-X."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005131; AAR8137.1; -.
DR HSSP; P53563; INF3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PSS0063; BH4_2; 1.
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match 43.6%; Score 439.5; DB 6; Length 233;
 Best Local Similarity 42.0%; Pred. No. 5,9e-31;
 Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADFGVYKLRQKGYC-----GAG-----GEGPAA 39
 DB 6 RELVADFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSALINGNPAMHADSAPV 65
 QY 40 D-----PLHQAMRAAGDEFETFRFRFTFSDLAOLHVTGSAQQRFTQ 81
 DB 66 NGATCHSSSLDAREVIPTMAVKQALREAGDEFELRYRRAFSDLTLSQHLITGTAYQSEBQ 125
 QY 82 VSDELFGQGPWMGRVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHSS 141
 DB 126 VVNELFPRDGVNMGRIVAFVFGAALCVESVDKEMVLSRIAAMWATYLNHLEPWIOEN 185
 QY 142 GGMAEFTALYDGALEEARLRLE--GNWASVRYTLTGAVALGAL 183
 DB 186 GGMDFTFVELYGNNAAESKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 7

035844 PRELIMINARY; PRT; 233 AA.

AC 035844; 01-JUN-1998 (TrEMBLrel. 05, Created)
 DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bcl-XL.
 GN BCL2L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus;
 RX MEDLINE=98051053; PubMed=9390687;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 RT apoptosis in T cells.";
 RT Immunol. 7:629-638(1997).
 RL EMBL; U51278; AAC33459.1; -
 DR HSP; P53563; IAF3.
 DR MGD; MGJ:88139; Bcl2L.
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0016329; P.apoptosis; IEA.
 DR GO; GO:0006915; P.apoptosis; IEA.
 DR GO; GO:0006915; P.apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH.
 DR InterPro; IPR004725; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PSS01080; BH1; 1.
 DR PROSITE; PSS01258; BH2; 1.
 DR PROSITE; PSS01259; BH3; 1.
 DR PROSITE; PSS01260; BH4; 1; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26033 MW; 3083FD8327E072E CRC64;

Query Match 43.2%; Score 435.5; DB 11; Length 233;
 Best Local Similarity 41.8%; Pred. No. 1.3e-30;
 Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADFGVYKLRQKGY-----V 28
 DB 6 RELVADFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSALINGNPAMHADSAPV 65

QY 29 CGAGPEGEPAAD-----PLHQAMRAAGDEFETFRFRFTFSDLAOLHVTGSAQQRFT 80
 DB 66 NGA-TGHSSSLDAREVIPTMAVKQALREAGDEFELRYRRAFSDLTLSQHLITGTAYQSEB 124
 QY 81 VSDELFGQGPWMGRVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHSS 140
 DB 125 QVNELFPRDGVNMGRIVAFVFGAALCVESVDKEMVLSRIAAMWATYLNHLEPWIOE 184
 QY 141 GGMAEFTALYDGALEEARLRLE--GNWASVRYTLTGAVALGAL 183
 DB 185 GGMDFTFVELYGNNAAESKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 8

088042 PRELIMINARY; PRT; 233 AA.

AC 088042; 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bcl-XL protein.
 GN BCL-XL.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;
 RT "Molecular cloning of feline Bcl-2 family.";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB080951; BAB85856.2; -
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0016329; P.apoptosis; IEA.
 DR GO; GO:0006915; P.apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH.
 DR InterPro; IPR004725; Bcl2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PSS01080; BH1; 1.
 DR PROSITE; PSS01258; BH2; 1.
 DR PROSITE; PSS01259; BH3; 1.
 DR PROSITE; PSS01260; BH4; 1; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 DR PROSITE; PSS0063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;

Query Match 42.9%; Score 432.5; DB 6; Length 233;
 Best Local Similarity 41.8%; Pred. No. 2.5e-30;
 Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;

QY 11 RALVADFGVYKLRQKGY-----V 28
 DB 6 RELVADFLSYKLSQKGYMSQPSDVENRTEAPEGTGEMETPSALINGNPAMHADSAPV 65
 QY 29 CGAGPEGEPAAD-----PLHQAMRAAGDEFETFRFRFTFSDLAOLHVTGSAQQRFT 80
 DB 66 NGA-TGHSSSLDAREVIPTMAVKQALREAGDEFELRYRRAFSDLTLSQHLITGTAYQSEB 124
 QY 81 VSDELFGQGPWMGRVAFVFGAALCAESVKNKEPVLGVQVQDMVAVLETRLADWTHSS 140
 DB 125 QVNELFPRDGVNMGRIVAFVFGAALCVESVDKEMVLSRIAAMWATYLNHLEPWIOE 184
 QY 141 GGMAEFTALYDGALEEARLRLEGNWASVRYTLTGAVALGALVGAFFASK 193
 DB 185 GGMDFTFVELYGNNAAESKQGERFNRWFLTGMTVAG-VLLGSLFSK 223

RESULT 9

OSN1A2

ID 09N1A2

PRELIMINARY;

PRT; 233 AA.

AC 09N1A2;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Anti-apoptotic regulator Bcl-XL.

GN BCL-XL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_Taxid=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RA Lee T.L., Cauty J.M.,

RT "PCR Cloning of a Porcine bcl-xl cDNA from Heart."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF216205; AAF33212.1; -.

DR HSSP: Q07817; IMAZ.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0016329; F:apoptosis regulator activity; IEA.

DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4_2; 1.

SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;

Query Match 42.8%; Score 431.5; DB 6; Length 233;

Best Local Similarity 41.8%; Pred. No. 3e-30;

Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

Db 11 RALVADFVGYKLRKQGY-----Y 28

Db 6 RELVADFVGYKLRKQGY-----Y 28

Db 29 CGAGPECEPAD-----PLHQAMRAAGDEFETFRRTFSDLAQLHTVPGSAQCRFT 80

Db 66 NGA-TGHSSSLDAREVYMAAVKQALREAGDEFELRYRASFDTLSQHLITGTAYQSF 124

QY 81 QVSDLEFGGPNWGRVAFVFGAALCAESVKNKEPVLGVQDMVAVLEFLADWHS 140

Db 125 QVNEIFRDGVWGRVAFVFGAALCAESVKNKEPVLGVQDMVAVLEFLADWHS 184

QY 141 SGMAEFTALYDGLAEARLRE--GNWASVRYLTGAVALGAL 183

Db 185 NGMDTFVELYGNNAAESRKQGRFNRWFLTGMTAGVLLGSL 229

RESULT 10

OSM2S7

ID 09M2S7

PRELIMINARY;

PRT; 233 AA.

AC 09M2S7;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Bcl-x long protein.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_Taxid=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;

RT "Bcl-x in the sheep ovary."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF164517; AAF89532.1; -.

DR HSSP: P53563; IAF3.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0016329; F:apoptosis regulator activity; IEA.

DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS50063; BH4_2; 1.

SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;

Query Match 42.5%; Score 428.5; DB 6; Length 233;

Best Local Similarity 40.6%; Pred. No. 5.e-30;

Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

Db 11 RALVADFVGYKLRKQGY-----VCGAP-----GEGPAA 39

Db 6 RELVADFVGYKLRKQGY-----VCGAP-----GEGPAA 39

QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAQLHTVPGSAQCRFTQ 81

Db 66 NGATGHSRLDAREVYMAAVKQALREAGDEFELRYRASFDTLSQHLITGTAYQSF 125

QY 82 VSDLEFGGPNWGRVAFVFGAALCAESVKNKEPVLGVQDMVAVLEFLADWHS 141

Db 126 VNEIFRDGVWGRVAFVFGAALCAESVKNKEPVLGVQDMVAVLEFLADWHS 185

QY 142 SGMAEFTALYDGLAEARLRE--GNWASVRYLTGAVALGAL 183

Db 186 NGMDTFVELYGNNAAESRKQGRFNRWFLTGMTAGVLLGSL 229

RESULT 11

OSBOK4

ID 08BOK4

PRELIMINARY;

PRT; 236 AA.

AC 08BOK4;

DT 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE B-cell leukemia/lymphoma 2.

GN BCL2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Body;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";

RL Nature 420:563-573 (2002).
 DR EMBL: AK049473; BAC33767.1; -
 DR MGD: MGI:88138; Bcl2.
 DR GO: GO:0005829; Cytosol; IDA.
 DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0006915; F:apoptosis; IDA.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 SQ SEQUENCE 236 AA; 26437 MW; B726BFA3A1C718 CRC64;

Query Match 40.8%; Score 412; DB 11; Length 236;
 Best Local Similarity 37.5%; Pred. No. 1.6e-28;
 Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;

QY 9 DTRALVADPVGKLRQKGVCGAG-----PG----- 34
 DB 10 DNRRLVATKXIKYKLSQRGYEMDAGDADAFLGAAPTFIFQPSNEMPAVHRDMAART 69
 QY 35 -----EGPADP-----LHQANRAAGDEFETFRRTFSDLAQLHTPTGSAQQRFTQ 81
 DB 70 SPLRLVATGTPALSPVPVPHVLTLRAGDDPSRYRDRPFAMSSQLHTPTFARGSPAT 129
 QY 82 VSDELFGGPNMGRVAFVFGAALCAESVNEKEPVLGVQVQDMVAVLETRLADWIHSS 141
 DB 130 VSEELFRDGVNMGRIYAFEFEGVNCVSVNREMSPLVDNIALMWTETYLNRHLHTWIDN 189
 QY 142 GGMAEFTALYDGALEEARLRREGNMAVSRTVLTGAVLALVTYGAFPAASK 193
 DB 190 GGMDFAVELVYG---PSMRPLDFSWLSIKTLISAL-VGACITLGAVALGSK 236

RESULT 12
 Q7TSN8 PRELIMINARY; PRT; 236 AA.
 AC Q7TSN8;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Bcl2-like protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar;
 RA Tanaka T., Nangaku M.;
 RT "Rat Bcl2-like protein."
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF512835; AAF47159.1; -
 SQ SEQUENCE 236 AA; 26407 MW; 80PDCBF78C735092 CRC64;

Query Match 40.8%; Score 412; DB 11; Length 236;
 Best Local Similarity 37.5%; Pred. No. 1.6e-28;
 Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;
 QY 9 DTRALVADPVGKLRQKGVCGAG-----PG----- 34
 DB 10 DNRRLVATKXIKYKLSQRGYEMDAGDADAFLGAAPTFIFQPSNEMPAVHRDMAART 69

QY 35 -----EGPADP-----LHQANRAAGDEFETFRRTFSDLAQLHTPTGSAQQRFTQ 81
 DB 70 SPLRLVATGTPALSPVPVPHVLTLRAGDDPSRYRDRPFAMSSQLHTPTFARGSPAT 129
 QY 82 VSDELFGGPNMGRVAFVFGAALCAESVNEKEPVLGVQVQDMVAVLETRLADWIHSS 141
 DB 130 VSEELFRDGVNMGRIYAFEFEGVNCVSVNREMSPLVDNIALMWTETYLNRHLHTWIDN 189
 QY 142 GGMAEFTALYDGALEEARLRREGNMAVSRTVLTGAVLALVTYGAFPAASK 193
 DB 190 GGMDFAVELVYG---PSMRPLDFSWLSIKTLISAL-VGACITLGAVALGSK 236

RESULT 13
 Q7TS61 PRELIMINARY; PRT; 79 AA.
 AC Q7TS61;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE BCL-WS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22672518; PubMed=12787069;
 RA Itoh T., Itoh A., Pleasure D.;
 RT "Bcl-2-related protein family gene expression during oligodendroglial
 RT differentiation."
 RL J. Neurochem. 85:1500-1512 (2003).
 DR EMBL: AY185099; AAO64469.1; -
 SQ SEQUENCE 79 AA; 8602 MW; 47EDFB3E2909485 CRC64;

Query Match 40.2%; Score 406; DB 11; Length 79;
 Best Local Similarity 98.7%; Pred. No. 1.4e-28;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 115 MEPLVGQVQDMVAVLETRLADWIHSSGGMAEFTALYDGALEEARLRREGNMAVSRTVLT 174
 DB 1 MEPLVGQVQDMVAVLETRLADWIHSSGGMAEFTALYDGALEEARLRREGNMAVSRTVLT 60
 QY 175 TGAVALGALVTYGAFPAASK 193
 DB 61 TGAVALGALVTYGAFPAASK 79

RESULT 14
 Q9BDS5 PRELIMINARY; PRT; 180 AA.
 AC Q9BDS5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Anti-apoptotic regulator Bcl-xL (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amills M., Bouzat U.;
 RT "Characterization of the bovine bcl-xL gene and related pseudogenes."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245489; AAK31307.1; -
 DR EMBL: AF245489; AAK31308.1; -
 DR HSP; Q07817; IMAZ.
 DR GO: GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO: GO:0006915; P:apoptosis; IEA.

DR InterPro; IPR000712; Bcl2_EH.
 DR InterPro; IPR002475; BCL2_family.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;

Query Match 39.7%; Score 401; DB 6; Length 180;
 Best Local Similarity 53.5%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFRFRFTSDLAQLHVTGSAQCRFTQVSDELFOGPPNGRLVAFVFG 103
 DB 38 QALREAGDEFEFLRYRRAFSDLTSQLHTPGTAQSFEOVNNELFRDGVNMGRIVAFFSFG 97
 QY 104 AALCAESVKNKEMEPYGVQVODMWVAYLETRLDWTHSSGMAEFTALYDGDALAEARLR 163
 DB 98 GALCVESVDKEMQVLSRIATWATYLDHLEPWTQENGMDTFVELYGNNAAESRKGQ 157
 QY 164 E--GNMASVRYTLTGAVALGAL 183
 DB 158 ERFNRWFLTGMTVAGVVLGSL 179

RESULT 15
 ID Q99N35 PRELIMINARY; PRT; 217 AA.

AC Q99N35;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE B-cell leukemia/lymphoma x (Fragment).
 GN BCLX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RA Yang X.-F.; Cantor H.;
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory
 RT gene Bcl-x-gamma";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF133282; AAK15455.1; -
 DR EMBL; AF133281; AAK15455.1; JOINED.
 DR HSSP; P53563; IAP3.
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0016329; Fapoptosis regulator activity; IEA.
 DR GO; GO:0006915; Fapoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_EH.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 FT NON_TER 1
 FT NON_TER 180
 SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match 39.7%; Score 401; DB 11; Length 217;
 Best Local Similarity 53.5%; Pred. No. 1.4e-27;
 Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;

QY 44 QAMRAAGDEFEFRFRFTSDLAQLHVTGSAQCRFTQVSDELFOGPPNGRLVAFVFG 103

DB 72 QALREAGDEFEFLRYRRAFSDLTSQLHTPGTAQSFEOVNNELFRDGVNMGRIVAFFSFG 131
 QY 104 AALCAESVKNKEMEPYGVQVODMWVAYLETRLDWTHSSGMAEFTALYDGDALAEARLR 163
 DB 132 GALCVESVDKEMQVLSRIATWATYLDHLEPWTQENGMDTFVDLYGNNAAESRKGQ 191
 QY 164 E--GNMASVRYTLTGAVALGAL 183
 DB 192 ERFNRWFLTGMTVAGVVLGSL 213

Search completed: March 25, 2004, 15:44:27
 Job time : 37 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: March 25, 2004, 15:36:20 ; Search time 14 Seconds
(without alignments)
1326.069 Million cell updates/sec

Title: US-09-155-327g-9
Perfect score: 1009
Sequence: 1 MATPASTPDRALVADPVGY.....LTGAVLGLATVGAFAASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 428.5 | 42.5 | 233 | 2 | bcl-x long - mouse |
| 2 | 427.5 | 42.4 | 233 | 2 | apoptosis regulato |
| 3 | 424.5 | 42.1 | 233 | 2 | bcl-x protein - ra |
| 4 | 423.5 | 42.0 | 233 | 2 | transforming prote |
| 5 | 414 | 41.0 | 232 | 2 | transforming prote |
| 6 | 411.5 | 40.8 | 239 | 1 | transforming prote |
| 7 | 411 | 40.7 | 236 | 1 | BCR-2 - rat (fragm |
| 8 | 406 | 40.2 | 236 | 2 | Gene bcl-2 protein |
| 9 | 405 | 40.1 | 236 | 1 | transforming prote |
| 10 | 404.5 | 40.1 | 233 | 2 | BCR-X-long - rat |
| 11 | 402 | 39.8 | 236 | 2 | B-cell lymphoma 2 |
| 12 | 378 | 37.5 | 190 | 2 | apoptosis regulato |
| 13 | 377.5 | 37.4 | 214 | 2 | bcl-x transmembran |
| 14 | 374.5 | 37.1 | 227 | 2 | apoptosis regulato |
| 15 | 356 | 35.3 | 216 | 2 | transforming prote |
| 16 | 348.5 | 34.5 | 199 | 1 | transforming prote |
| 17 | 345 | 34.2 | 205 | 1 | transforming prote |
| 18 | 277.5 | 27.5 | 154 | 2 | gene bcl-2 protein |
| 19 | 182 | 18.0 | 170 | 2 | gene bcl-x short - |
| 20 | 174 | 17.2 | 176 | 2 | gene bcl-x short pr |
| 21 | 171 | 16.9 | 211 | 2 | Bak protein - huma |
| 22 | 168 | 16.7 | 211 | 2 | cdh-2 protein - hu |
| 23 | 158.5 | 15.7 | 192 | 2 | bcl-2-associated p |
| 24 | 154 | 15.3 | 192 | 2 | bcl-2-associated p |
| 25 | 151 | 15.0 | 261 | 2 | apoptosis suppress |
| 26 | 150.5 | 14.9 | 133 | 2 | bcl-2-associated p |
| 27 | 147.5 | 14.6 | 179 | 2 | Bax-related protein |
| 28 | 147.5 | 14.6 | 218 | 2 | bcl-2-associated p |
| 29 | 147.5 | 14.6 | 218 | 2 | bcl-2-associated p |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 142 | 14.1 | 177 | 2 | S54778 | NR-13 protein - qu |
| 31 | 138.5 | 13.7 | 143 | 2 | I38921 | bcl-2-associated p |
| 32 | 138 | 13.7 | 255 | 2 | UC7567 | Mcl-1a protein - z |
| 33 | 116 | 11.5 | 175 | 2 | I39055 | bcl-2 related - hu |
| 34 | 116 | 11.5 | 350 | 2 | A47476 | BCL2 homolog MCL1 |
| 35 | 105 | 10.4 | 172 | 2 | I49449 | hemopoietic-specif |
| 36 | 88 | 8.7 | 185 | 2 | B83217 | hypothetical prote |
| 37 | 87 | 8.6 | 343 | 1 | GNWYXV | genome polyprotein |
| 38 | 86.5 | 8.6 | 301 | 2 | T36534 | probable lipase/es |
| 39 | 86 | 8.5 | 270 | 2 | A12598 | dihydrodipicolinat |
| 40 | 86 | 8.5 | 279 | 2 | B97381 | dihydrodipicolinat |
| 41 | 84.5 | 8.4 | 358 | 1 | AULCQB | glutamate--ammonia |
| 42 | 83.5 | 8.3 | 872 | 2 | G98026 | alanine-tRNA ligas |
| 43 | 83.5 | 8.3 | 872 | 2 | H95160 | alanyl-tRNA synthe |
| 44 | 83 | 8.2 | 3430 | 1 | GNWYV | genome polyprotein |
| 45 | 81.5 | 8.1 | 886 | 2 | A32758 | beta-amyloid-like |

ALIGNMENTS

RESULT 1
149056
bcl-x long - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C/Accession: I49056; S52866
R/Fang, W.; Rivard, J.U.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4368-4398, 1994
A/Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A/Reference number: I49055; NCID:95052604; PMID:7963517
A/Accession: I49056
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-233 <RES>
A/Reference: EMBL:U0101; NID:9506647; PIDN:AAA82173.1; PID:9506648
R/Kameaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
Submitted to the EMBL Data Library, November 1994
A/Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throu
A/Reference number: S52866
A/Accession: S52866
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-233 <RAM>
A/Reference: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 42.5%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.2e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

| | | | |
|----|-----|--|------|
| QY | 11 | RALVADPVGYKLEOKGY----- | V 28 |
| DB | 6 | RELVDPLSYKLSQKGYSSQPSVDENETPAEETPAEETPSALNGNPSWHLADSPAV 65 | |
| QY | 29 | CGAGPEGEPAD-----PLHOANRAAGDFFETFRFTFDLAOLHVTGSAQOQRT 80 | |
| DB | 66 | NGA-TGHSSSLDAREVTPMAAVQALREAGDEBELRRASFDLTSLHTITGTAVQSPF 124 | |
| QY | 81 | QVDELFQGGPWNKRLVAFVFGAALCAASVKNKEPEPLVGYQVODMVALEFRIDWITS 140 | |
| DB | 125 | QVNEELFRGQVWNGRLVAFVFGAALCAASVKNKEPEPLVGYQVODMVALEFRIDWITS 184 | |
| QY | 141 | SGGMAEFTLLYDGALEBARLRE--GNMAYRTVLTGAVLGLAL 183 | |
| DB | 185 | NGGMDTFVDLYGNMAAASRKQGERFRNRFLLTGMVAVGLLGLSL 229 | |

RESULT 2
B47537
apoptosis regulator bcl-xl - human
N/Alternate names: bcl-2-related protein
N/Contains: apoptosis regulator bcl-xs

C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
C:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turkka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-2, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: B47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <B01>
A:Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
A:Accession: C47537
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69, 'G', '71-125, 189-233 <B02>
A:Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C:Genetics:
A:Gene: GDB:BCU2L
A:Cross-references: GDB:228079
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis
F:1-233/Product: apoptosis regulator bcl-XL #status predicted <MAT>
F:1-125, 189-233/Product: apoptosis regulator bcl-XS #status predicted <MA2>

Query Match 42.4%; Score 427.5; DB 2; Length 233;
Best Local Similarity 40.6%; Pred. No. 2.8e-32;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

QY 11 PALVADPVGKLRQKGY-----VCGNPG---GEPPAA 39
DB 6 RELVDFLSTYLSQKGYSMQSPDVEENRTEAPGTESEMETPSAINGNPSMHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRRFRFSDLAQHLVTPGSAQGRFTQ 81
DB 66 NGATRAHSSLDAREVTPMAAVKQALREAGDEFELRRRAFSDDLTSQHLITPGINVSFEQ 125
QY 82 VSEDFQGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAVLETRLDWVHSS 141
DB 126 VVNEIFRQGVNMGRIIVAFSFGALCVESVDKEMQVLSRAAMATLNDHLEPWIOEN 185
QY 142 GGMAEFTALYDGALEEARLRE--GNMASVTVLTGAVALGAL 183
DB 186 GMDTFVLDYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 3
S51761
BCL-X protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 26-Jul-2003
C:Accession: S51761; S51762
R:Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A:Reference number: S51761
A:Accession: S51761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MIC>
A:Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; P-ID:g607177
A:Experimental source: embryonic; brain
A:Accession: S51762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125, 189-233 <MI2>
A:Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; P-ID:g607178
A:Experimental source: embryonic; brain
A:Note: smaller form due to splicing
C:Genetics:
A:Insertions: 125/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
Query Match 42.1%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 5.3e-32;
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;
QY 13 LVADPVGKLRQKGY-----VCG 30
DB 8 LVADFLSTYLSQKGYSMQSPDVEENRTEAPEETEPETPSAINGNPSMHLADSPAVNG 67
QY 31 ACPGSGPAD-----PLHQAMRAAGDEFETRRFRFSDLAQHLVTPGSAQGRFTQ 82
DB 68 A-TGHSSSLDAREVTPMAAVKQALREAGDEFELRRRAFSDDLTSQHLITPGINVSFEQ 126
QY 83 SEELFQGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAVLETRLDWVHSSG 142
DB 127 VVNEIFRQGVNMGRIIVAFSFGALCVESVDKEMQVLSRAAMATLNDHLEPWIOEN 186
QY 143 GMAEFTALYDGALEEARLRE--GNMASVTVLTGAVALGAL 183
DB 187 GMDTFVLDYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 4
A37332
transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C:Accession: A37332; S35453
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: A37332
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-233 <EGU>
A:Cross-references: EMBL:D11381
C:Genetics:
A:Insertions: 189/3
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 42.0%; Score 423.5; DB 2; Length 233;
Best Local Similarity 38.0%; Pred. No. 6.5e-32;
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;
QY 9 DFRALVADPVGKLRQKGYVCGAG-----PGSGPADP----- 41
DB 10 DNRFLVKTITHTKLSQKGYDMDAGDEDRPPAPAPAPAAVAAAGASSHHRRPPGSA 69
QY 42 -----LHQAMRAAGDEFETRRFRFSDLAQHLVTPGSAQGRFTQ 84
DB 70 AASEVPPAGELPAPPGVHALRQAGDEFRRYQDFAQMSQHLTFTHAGRVAAVE 129
QY 85 ELFGGPNMGRIVAFVFGALCAESVKNEMEPVGVQVDMVAVLETRLDWVHSSG 144
DB 130 ELFRDGVNMGRIIVAFSFGALCVESVDKEMQVLSRAAMATLNDHLEPWIOEN 189
QY 145 AEFTALYDGALEEARLREGNMASVTVLTGAVALGAVTGAPFASK 193
DB 190 DAFVELYGN-----SNRPLDFSMISLKTILS-LVVGACITLGAAYLGHK 233

RESULT 5
S24390
transforming protein (bcl-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 28-Jul-2003
C:Accession: S24390
R:Caizals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A:Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-232 <CA6>
 A:Cross-references: EMBL:Z11961; NID:G62969; PIDD:CAA78018.1; PID:G62970
 C:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: mitochondrion; transmembrane protein

Query Match 41.0%; Score 414; DB 2; Length 232;
 Best Local Similarity 37.7%; Pred. No. 4.9e-31;
 Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADPFVGYKLRQKGYVCGAG-----PGEGPADP----- 41
 DB 10 DNRRLVWKYHKLKSGRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHPAASRDVART 69
 QY 42 -----LHOAMRAAGDEFEFTRFRRTFSDLAAQLHVTGSAOQRTQVSD 85
 DB 70 LTVRCPLRGCAAPGVHLLTRQAGDDFERRYRDRPAEMWSQHLTPFATGRFAVVEE 129
 QY 86 LFGGPNMGRVLAFFVFGAALCAESVKNKEMEPVGVQVDMVAAYLETPLADMIHSSGMA 145
 DB 130 LFRDGVNWRIVAFEFEGVWCVESVNRBMSPVLDNIMTMTTEYLNRHLHWIQQNGSMD 189
 QY 146 EFTALVGDGALBEARLRREGNMAVSTVLTGVALGALVTVGAFPAFSK 193
 DB 190 AFVELYGN-----PSMRPLDFPWSLTKTLIS-LVVGACITLGAIVGHK 232

RESULT 6

TVHUAL
 transforming protein bcl-2, splice form alpha - human

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text_change 28-Jul-2003
 C/Accession: C37332; A29409; S02452; A24428; A27622; B27622
 R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A>Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A:Reference number: A37332; PMID:92375724; PMID:1508712
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-239 <EGU>
 A>Note: this report is a correction
 R/Tsujimoto, Y.; Croce, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A>Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for Burkitt's lymphoma
 A:Reference number: A29409; PMID:86259760; PMID:3523487
 A:Accession: A29409
 A:Molecule type: mRNA
 A:Residues: 1-95, 'A', '97-109, 'G', '111-236, 'S', '238-239 <TSU>
 A:Cross-references: GB:M13994; NID:G179366; PIDD:AAA51813.1; PID:G179367
 A>Note: this sequence has been corrected in reference A37332
 R/Seeto, M.; Jaeger, U.; Hockett, R.D.; Granger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
 EMBO J. 7, 123-131, 1988
 A>Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene in human B-cell lymphomas
 A:Reference number: S02452; PMID:88196071; PMID:2834197
 A:Accession: S02452
 A:Molecule type: mRNA
 A:Residues: 1-239 <SET>
 R/Cleary, M.L.; Smith, S.D.; Sklar, J.
 Cell 47, 19-28, 1986
 A>Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer gene (IGHV)
 A:Reference number: A24428; PMID:87002488; PMID:2875799
 A:Accession: A24428
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', '60-116, 'R', '118-239 <CLE>
 A:Cross-references: GB:M14745; NID:G179370; PIDD:AAA5591.1; PID:G179371
 R/Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.D.; Bakshi, A.
 Oncogene Res. 2, 263-275, 1988
 A>Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: a study of 100 cases
 A:Reference number: A27622; PMID:88217344; PMID:3285301
 A:Accession: A27622
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', '60-239 <HUA>

A:Accession: B27622

A:Molecule type: DNA
 A:Residues: 1-6, 'S', '8-58, 'T', '60-128, 'C', '130-239 <HUA2>
 A>Note: the sequence was determined from the germline gene
 C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
 C:Genetics:
 A:Gene: GDB:BCL2
 A:Cross-references: GDB:119031; OMIM:151430
 A:Map position: 18q21.3-18q21.3
 C:Function:
 A:Description: blocks apoptosis in hematopoietic cells
 A:Superfamily: bcl apoptosis regulator, inhibitory type
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto-oncogene

Query Match 40.8%; Score 411.5; DB 1; Length 239;
 Best Local Similarity 37.0%; Pred. No. 8.8e-31;
 Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADPFVGYKLRQKGYVCGAG-----PGEGPADP----- 35
 DB 10 DNRRLVWKYHKLKSGRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHPAASRDVART 69
 QY 36 -----GPAADP-----LHOAMRAAGDEFEFTRFRRTFSDLAAQLHVTGSAOQ 78
 DB 70 SPLTPAAPGAAGPALSPVPVHLLTRQAGDDFERRYRDRPAEMWSQHLTPFATGR 129
 QY 79 FTVSDLEFQGGPNMGRVLAFFVFGAALCAESVKNKEMEPVGVQVDMVAAYLETPLADMI 138
 DB 130 FATVELEFEDGVNWRIVAFEFEGVWCVESVNRBMSPVLDNIMTMTTEYLNRHLHWIQQNGSMD 189
 QY 139 HSSGMAEFPLVGDGALBEARLRREGNMAVSTVLTGVALGALVTVGAFPAFSK 193
 DB 190 QDGMDFVELYGN-----PSMRPLDFPWSLTKTLISL-LVVGACITLGAIVGHK 239

RESULT 7

167432
 BCL-2 - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change 28-Jul-2003
 C/Accession: 167432
 R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
 constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.
 A:Reference number: 153295; PMID:95129487; PMID:7828536
 A:Accession: 167432
 A:Status: preliminary; translated from GB/EMBL/DDBL
 A:Molecule type: mRNA
 A:Residues: 1-236 <RES>
 A:Cross-references: EMBL:U34964; NID:G1004378; PIDD:AAA77687.1; PID:G1004379
 C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 40.7%; Score 411; DB 2; Length 236;
 Best Local Similarity 36.2%; Pred. No. 9.6e-31;
 Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADPFVGYKLRQKGY-----PGEGPADP----- 27
 DB 10 DNRRLVWKYHKLKSGRGYEMDAGDVGAAPPGAAAPGIFSSQPGHTPHPAASRDVART 69
 QY 28 -----VCGAGPGGPAADPLHOAMRAAGDEFEFTRFRRTFSDLAAQLHVTGSAOQRTQ 81
 DB 70 SPLRPVYANGPALSPVPVHLLTRQAGDDFERRYRDRPAEMWSQHLTPFATGRFAT 129
 QY 82 VSDLEFQGGPNMGRVLAFFVFGAALCAESVKNKEMEPVGVQVDMVAAYLETPLADMIHSS 141
 DB 130 VBELEFEDGVNWRIVAFEFEGVWCVESVNRBMSPVLDNIMTMTTEYLNRHLHWIQQNGSMD 189
 QY 142 GGMNPFPLVGDGALBEARLRREGNMAVSTVLTGVALGALVTVGAFPAFSK 193
 DB 190 QDGMDFVELYGN-----PSMRPLDFPWSLTKTLISL-LVVGACITLGAIVGHK 236

A:Gene: bcl-2
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: B-cell lymphoma; ovary

Query Match 39.8%; Score 402; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 6.6e-30;
Matches 82; Conservative 34; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADFGVYKLRQKGY----- 27
DB 10 DNRREIMKXIKHYKLSRGKEMVDGVDAPLGAAPTPGFSQSPESNTPPAHDMART 69
QY 28 -----VCGAGPGEAPADPLHQAQAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQ 81
DB 70 SPURPVIATGPTLSPVPVHLLTRAGDDPSRRYRDPFAEMSQLHLPTFARGPRAT 129
QY 82 VDELFQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 141
DB 130 VVEELFRDGVNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 189
QY 142 GGAAEFALYGCALAEARLRGNWASVTVLTGVALGALVTGAPFASK 193
DB 190 GGWDAFVELYG---PSVRPLDFPFSWLSKTLISLAL-VGACITTYGTYLGHK 236

RESULT 12

A47537
apoptosis regulator bcl-x - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C:Accession: A47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turkka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: A47537
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <BOI>
A:Cross-references: GB:J23110; GB:J20120; NID:9510896; PIDN:CAA80657.1; PID:9510899
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.5%; Score 378; DB 2; Length 190;
Best Local Similarity 43.8%; Pred. No. 8.6e-28;
Matches 81; Conservative 14; Mismatches 44; Indels 46; Gaps 3;

QY 11 RALVADFGVYKLRQKGY-----VCGAGPGEAP----- 37
DB 6 RELVIDFVSYKLSQRCHCSELEEDENRTDAAEKMSVANGSWMHPPAGHYVNGAT 65
QY 38 -----AADPLHQAQAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQVSD 85
DB 66 VRRSSLEVEHEIVRASDVQRALRDAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQVSD 125
QY 86 LQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 145
DB 126 LPHDGVNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 185
QY 146 EFTAL 150
DB 186 R-TAL 189

RESULT 13

I49057
bcl-x transmembrane deleted - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2003
C:Accession: I49057
R:Farag, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49057; MUID:95032604; PMID:7963517

A:Accession: I49057
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-214 <RES>
A:Cross-references: EMBL:U10102; NID:9506649; PIDN:AA82174.1; PID:9506650
C:Genetics:
A:Gene: bcl-x-long
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.4%; Score 377.5; DB 2; Length 214;
Best Local Similarity 42.8%; Pred. No. 1.1e-27;
Matches 80; Conservative 16; Mismatches 40; Indels 51; Gaps 3;

QY 11 RALVADFGVYKLRQKGY-----V 28
DB 6 RELVIDFVSYKLSQRCHCSELEEDENRTDAAEKMSVANGSWMHPPAGHYVNGAT 65
QY 29 CGAGPGEAPAD-----PLHQAQAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQ 80
DB 66 NGA-TGHSSSIDAREVLPMAAVQALREAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQ 124
QY 81 QVSDLEFQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 140
DB 125 QVNNELFRDGVNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 184
QY 141 SGWAEF 147
DB 185 NGWMTF 191

RESULT 14

JE0203
apoptosis regulator bcl-x isoform - human
N:Alternate names: h-bcl-xbeta
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
C:Accession: JE0203
R:Ban, J.; Bokhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A:Reference number: JE0203; MUID:98340865; PMID:9675101
A:Accession: JE0203
A:Molecule type: mRNA
A:Residues: 1-227 <BAN>
A:Cross-references: GB:U72398; NID:91622940; PIDN:AA817354.1; PID:91622941
C:Genetics:
A:Gene: bcl-x
A:Map position: 20
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 37.1%; Score 374.5; DB 2; Length 227;
Best Local Similarity 40.8%; Pred. No. 2.3e-27;
Matches 82; Conservative 18; Mismatches 50; Indels 51; Gaps 3;

QY 11 RALVADFGVYKLRQKGY-----V 28
DB 6 RELVIDFVSYKLSQRCHCSELEEDENRTDAAEKMSVANGSWMHPPAGHYVNGAT 65
QY 29 CGAGPGEAPAD-----PLHQAQAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQ 80
DB 66 NGA-TGHSSSIDAREVLPMAAVQALREAGDEFEFRFRRTFSDLAAQLHYTPGSAQORFTQ 124
QY 81 QVSDLEFQGGPNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 140
DB 125 QVNNELFRDGVNMGRIVAFVFGAALCAESVKNEMEPVGVQVQDMMVAYLETRADWHS 184
QY 141 SGWAEFALYGCALAEARLRGNWASVTVLTGVALGALVTGAPFASK 161
DB 185 NGWMTFPLVCPFSLASGOR 205

RESULT 15

B3732

transforming protein (bcl-2-beta) - chicken

C;Species: Gallus gallus (chicken)

C:\Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003

C;Accession: B37332; S35452

R; Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A; Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie

A;Reference number: A37332; MUID:92375724; PMID:15087124

A;Accession: B37332

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-216 <EGU>

A;CROSS-references: EMBL:D11381; EMBL:D11382

C;Superfamily: bcl apoptosis regulator, inhibitory type

| | | | | |
|-----------------------|--------|--------------------|----------------|-------------|
| Query Match | 35.3%; | Score 356; | DB 2; | Length 216; |
| Best Local Similarity | 38.4%; | Pred. No. 1.1e-25; | | |
| Matches | 71; | Conservative 21; | Mismatches 49; | Indels 44; |
| | | | | Gaps 2; |

```

Oy      9  DTRLVADPFGYKLRQGYVCCAG-----GGEAGADP-----41
Db      10 DNRETVLKTHYKLSQRGYDMAAGEDRPVPVPAPAPAPAPAAVLAAGASHHREPPGSA 69

Oy      42 -----LHOAMPAGDEFEFRRTFSDLAQLHTVPSAQOOFVSD 84
Db      70 AASEVPAPAEGLRAPPCGVHIALRQAQDEFSRRYQRFDAQMSQHLTPFTHAGFVAVE 129

Oy      85 ELFEGGNNMGRLLVAFVYFGAALCAESVUNKEMBEVLGVQVDMVAVLETRLADWTHSSGW 144
Db      130 ELFFEDGYNMGRIVAFPEFGVCMCVESVNMREMSPLVDNIATWTEYLNHNLNMIQDNGW 189

Oy      145 AEFYA 149
Db      190 VRACA 194

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Search completed: March 25, 2004, 15:45:07
Job time : 15 secs

CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA;
Query Match 100.0%; Score 1009; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.4e-102;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGSPADPLHQAMRAAGDEFETRRPT 60
DB 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGSPADPLHQAMRAAGDEFETRRPT 60
QY 61 FSDLAALHTVTPGSAQGRFTQVSDELFOGGPNWGRVAFVFGAALCAESVKNKEPLVG 120
DB 61 FSDLAALHTVTPGSAQGRFTQVSDELFOGGPNWGRVAFVFGAALCAESVKNKEPLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYGDALAEARLRREGNMAVTRVLTGAVAL 180
DB 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYGDALAEARLRREGNMAVTRVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193
RESULT 2
AAM61391
ID AAM61391 standard; protein; 193 AA.
XX
AC AAM61391;
XX
DN 02-OCT-1998 (first entry)
DT
XX
DE Rat bcl-y protein.
XX
KM bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR N-PSDB; AAV28333.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
PT
PS Example; Fig 3A; 27pp; English.
XX
CC The mammalian bcl-y protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 193 AA;
Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 2e-101;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGSPADPLHQAMRAAGDEFETRRPT 60
DB 1 MATPASTPDRALVADVGVYKLRQKGYVCGAGGEGSPADPLHQAMRAAGDEFETRRPT 60
QY 61 FSDLAALHTVTPGSAQGRFTQVSDELFOGGPNWGRVAFVFGAALCAESVKNKEPLVG 120
DB 61 FSDLAALHTVTPGSAQGRFTQVSDELFOGGPNWGRVAFVFGAALCAESVKNKEPLVG 120
QY 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYGDALAEARLRREGNMAVTRVLTGAVAL 180
DB 121 QVQDMWVAVLETRLADWIIHSSGGMAEFTALYGDALAEARLRREGNMAVTRVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193
RESULT 3
AAM97391
ID AAM97391 standard; protein; 193 AA.
XX
AC AAM97391;
XX
DN 20-MAY-1999 (first entry)
DT
XX
DE The rat bcl-y protein.
XX
KM Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Rattus sp.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR N-PSDB; AAX15945.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
PT
PS Disclosure; Col 15-18; 26pp; English.
XX
CC The present sequence represents rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended

CC period. In contrast, if they act as cell death stimulators, Bcl-1-y and
CC Hbcl-1-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
SQ Sequence 193 AA;

Query Match 99.6%; Score 1005; DB 2; Length 193;
Best Local Similarity 99.5%; Pred. No. 2e-101;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFYGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60
DB 1 MATPASTPTDTRALVADFYGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESYNKMEPLVQ 120
DB 61 FSDLAQLHVTGPSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESYNKMEPLVQ 120
QY 121 QVQDMWVAVLETRLDWVHSSGGWAEFTALYGDGALBEARRLREGWNASVRTVLTGAVAL 180
DB 121 QVQDMWVAVLETRLDWVHSSGGWAEFTALYGDGALBEARRLREGWNASVRTVLTGAVAL 180
QY 181 GALVTGAFPAASK 193
DB 181 GALVTGAFPAASK 193

RESULT 4
AAW97393
AAW97393 standard; protein; 192 AA.

AC AAW97393;
DT 20-MAY-1999 (first entry)

DE Protein sequence of the specification.

KM Rat bcl-y protein; Bcl-1-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KM multiple sclerosis; myocardial infarction; vitally induced cell death;
KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM premature cell death; cell death stimulator; prolonged cell life span;
KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

XX Unidentified.

XX OS

XX PN

XX US5883229-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-00978523.

XX 23-FEB-1996; 96US-0012201P.

XX 11-FEB-1997; 97US-00798897.

XX (COCR-) COCENSYS INC.

XX Guastella J;

XX WPI; 1999-214150/18.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for

XX modulating programmed cell death.

CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent. They
CC may also be used in this way to develop cell lines which remain viable in
CC culture for an extended period. In contrast, if they act as cell death
CC stimulators, Bcl-1-y and Hbcl-1-y may be used to treat conditions associated
CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma
CC and lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites
SQ Sequence 192 AA;

Query Match 99.1%; Score 1000; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 7.1e-101;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATPASTPTDTRALVADFYGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 61
DB 1 ATPASTPTDTRALVADFYGYKLRQKGYVCGAGPGEGPADPLHQAMRAAGDEFETRFRRT 60
QY 62 SDLAQLHVTGPSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESYNKMEPLVQ 121
DB 62 SDLAQLHVTGPSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESYNKMEPLVQ 120
QY 122 QVQDMWVAVLETRLDWVHSSGGWAEFTALYGDGALBEARRLREGWNASVRTVLTGAVAL 181
DB 122 QVQDMWVAVLETRLDWVHSSGGWAEFTALYGDGALBEARRLREGWNASVRTVLTGAVAL 180
QY 182 ALVTGAFPAASK 193
DB 182 ALVTGAFPAASK 192

RESULT 5
AAV05530
AAV05530 standard; protein; 193 AA.

AC AAV05530;

DT 05-JUN-1999 (first entry)

DE Human Bcl-w protein essential for spermatogenesis.

KM Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;

XX animal model.

XX OS

XX Homo sapiens.

XX MO9913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-A0000764.

XX 16-SEP-1997; 97AU-00009228.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Cory S, Adams J, Print C, Gibson L, Koentgen F;

XX WPI; 1999-243890/20.

XX N-PEDB; AAX25132.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

CC protein associated with Bcl-w.

XX Claim 2; Page 33; 52pp; English.

XX The present sequence is human Bcl-w, a pro-survival member of the Bcl-2

CC family which is widely expressed and which is essential for
CC spermatogenesis. The invention relates generally to a method of treatment
CC and to an animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries a
CC mutation is at least one allele of the human or murine bcl-w gene (see
CC AX25133-35) or in a gene associated with bcl-w. Such animals have
CC disorganised seminiferous tubules and are substantially infertile, but
CC possess no other major abnormalities as determined by histological
CC examination. They can be used to screen for therapeutic molecules
CC including genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce infertility
XX
SQ Sequence 193 AA:

Query Match 99.1%; Score 1000; DB 2; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQARRAGDEFTFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQARRAGDEFTFRRT 60
QY 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGGPNMGRVAFVFGAALCAESVKNEMEPLVG 120
DB 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGGPNMGRVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWHSGGWAEFTALYGDGALIEARLRREGWASVRYTLTGAVAL 180
DB 121 QVQDMWVAYLETRLADWHSGGWAEFTALYGDGALIEARLRREGWASVRYTLTGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 6
ADD46742
ID ADD46742 standard; protein; 193 AA.

XX AC ADD46742;

DT 29-JAN-2004 (first entry)

XX Human Protein Q92843, SEQ ID NO 12427.

DE Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003016475-A2.

PN 27-FEB-2003.

PD 14-AUG-2002; 2002MO-US025765.

PF 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; Q92843.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIGO at
XX ftp.wigo.int/pub/published_pct_sequences.

SQ Sequence 193 AA:

Query Match 99.1%; Score 1000; DB 7; Length 193;
Best Local Similarity 99.0%; Pred. No. 7.1e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPPTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQARRAGDEFTFRRT 60
DB 1 MATPASAPDTRALVADPVGYKLRQKGYVCGAGGEGBPADPLHQARRAGDEFTFRRT 60
QY 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGGPNMGRVAFVFGAALCAESVKNEMEPLVG 120
DB 61 FSDLAQLHTVTPGSAQCRFTQVSDELFOGGPNMGRVAFVFGAALCAESVKNEMEPLVG 120
QY 121 QVQDMWVAYLETRLADWHSGGWAEFTALYGDGALIEARLRREGWASVRYTLTGAVAL 180
DB 121 QVQDMWVAYLETRLADWHSGGWAEFTALYGDGALIEARLRREGWASVRYTLTGAVAL 180
QY 181 GALVTVGAFPAK 193
DB 181 GALVTVGAFPAK 193

RESULT 7
AAW61392
ID AAW61392 standard; protein; 193 AA.

XX AC AAW61392;

DT 02-OCT-1998 (first entry)

DE Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

XX US5789201-A.

XX 04-AUG-1998.

XX 11-FEB-1997; 97US-00798897.

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XX 23-FEB-1996; 96US-0012201P.
XX PR (COCE-) COCENSYS INC.
XX PA
XX PI Guastella J;
XX DR WPI; 1998-446079/38.
XX DR N-PSDB; AAV28334.
XX PT Nucleic acids encoding B-cell lymphoma-Y protein - useful for producing
XX PT recombinant protein for use in treating uncontrolled cell growth e.g.
XX PT cancers.
XX PS Example; Column 17/18; 27bp; English.
XX CC The mammalian bcl-y protein is a member of the bcl-2 family, components
XX CC in the cell death pathway. The bcl-2 family have both apoptotic activity
XX CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
XX CC activity category. The recombinant protein may be used to prevent
XX CC uncontrolled cell growth, either by its direct administration to
XX CC recombinant genetic constructs to increase its expression in vivo. Also,
XX CC antisense constructs can be used in disorders where prevention of cell
XX CC death is desired.
XX SQ Sequence 193 AA;
XX
XX Query Match 98.6%; Score 995; DB 2; Length 193;
XX Best Local Similarity 98.4%; Pred. No. 2.5e-100;
XX Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPGEGPADPLHQAMRAAGDEFETFRRT 60
XX DB 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPGEGPADPLHQAMRAAGDEFETFRRT 60
XX
XX QY 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPVLG 120
XX DB 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPVLG 120
XX
XX QY 121 QVQDMVAVYLETRLADWVHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
XX DB 121 QVQDMVAVYLETRLADWVHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
XX
XX QY 181 GALVTGGAFFASK 193
XX DB 181 GALVTGGAFFASK 193
XX
XX RESULT 8
XX AAM97392
XX ID AAM97392 standard; protein; 193 AA.
XX AC AAM97392;
XX XX
XX DT 20-MAY-1999 (first entry)
XX DE The human bcl-y protein.
XX
XX Rat bcl-y protein; Hbcl-Y; human bcl-y protein; Hbcl-Y; bcl-2 homologue;
XX KM programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX KM head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
XX KM multiple sclerosis; myocardial infarction; vitally induced cell death;
XX KM aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
XX KM premature cell death; cell death stimulator; prolonged cell life span;
XX KM Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX OS Homo sapiens.
XX PN US5883229-A.
XX XX 16-MAR-1999.
XX PD
XX PF 25-NOV-1997; 97US-00978523.

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XX 23-FEB-1996; 96US-0012201P.
XX PR 11-FEB-1997; 97US-00798897.
XX PA (COCE-) COCENSYS INC.
XX PI Guastella J;
XX DR WPI; 1999-214150/18.
XX DR N-PSDB; AAX15946.
XX PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
XX PT modulating programmed cell death.
XX PS Claim 1; Col 17-18; 26bp; English.
XX CC The present sequence represents human bcl-y protein (Hbcl-Y). The
XX CC specification also describes rat bcl-y protein (Rbcl-Y). Rbcl-Y and Hbcl-
XX CC y are homologues of the bcl-2 protein thought to be involved in
XX CC programmed cell death (apoptosis and necrosis). Rbcl-Y and Hbcl-Y
XX CC proteins may be used to treat conditions associated with a disruption of
XX CC the cell death pathway. If they act as cell death inhibitors, they may be
XX CC used in therapies to treat subjects suffering from: strokes, head trauma,
XX CC Alzheimer's disease, neural and muscular degenerative diseases
XX CC (especially multiple sclerosis), myocardial infarction, vitally induced
XX CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
XX CC - conditions where cells under go premature cell death as a result of
XX CC triggers which may or may not be apparent. They may also be used in this
XX CC way to develop cell lines which remain viable in culture for an extended
XX CC period. In contrast, if they act as cell death stimulators, Rbcl-Y and
XX CC Hbcl-Y may be used to treat conditions associated with prolonged cell
XX CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
XX CC and auto/hyperimmune diseases. They may also be used to cause cell death
XX CC in, and hence control, parasites
XX SQ Sequence 193 AA;
XX
XX Query Match 98.6%; Score 995; DB 2; Length 193;
XX Best Local Similarity 98.4%; Pred. No. 2.5e-100;
XX Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPGEGPADPLHQAMRAAGDEFETFRRT 60
XX DB 1 MATPASPTDTRALVADPFVGYKLRQKGYCGAGPGEGPADPLHQAMRAAGDEFETFRRT 60
XX
XX QY 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPVLG 120
XX DB 61 FSDLAQLHTVTPGSAQORFTQVSDLEFGGPNWGRVAFVFGAALCAESVNMKEPVLG 120
XX
XX QY 121 QVQDMVAVYLETRLADWVHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
XX DB 121 QVQDMVAVYLETRLADWVHSSGWAFFETALYGDALBEARLRBGNMASVRYTLTGAVAL 180
XX
XX QY 181 GALVTGGAFFASK 193
XX DB 181 GALVTGGAFFASK 193
XX
XX RESULT 9
XX AAM36047
XX ID AAM36047 standard; protein; 193 AA.
XX AC AAM36047;
XX XX
XX DT 22-APR-1998 (first entry)
XX DE Human bcl-w protein.
XX
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
XX KM diagnosis; degenerative disease.
XX OS Homo sapiens.

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PN WO9735971-A1.
 XX 02-OCT-1997.
 PD 27-MAR-1997; 97WO-AU000199.
 XX 27-MAR-1996; 96AU-00008965.
 PR (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PA Cory S, Adams JM, Gibson LM, Holmgren SP;
 PI WPI; 1997-489635/45.
 DR N-PSDB; AAT96577.
 XX
 PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative
 PT diseases.
 PS
 XX Claim 6; Page 48; 86pp; English.
 XX
 CC This sequence represents a novel human protein, bcl-w, encoded by the bcl
 CC -2 gene family and extracted from an adult brain library. This gene
 CC promotes cell survival, so its modulation is useful in treatment of
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
 CC ischemia, human immunodeficiency virus infection or in cell transplants.
 CC up-regulation of the gene can also be used to modify cell lines cultured
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
 CC and to increase survival of primary explants during genetic modification.
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
 CC antibody production or screening of potential modulators
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 4.2e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADVGVYKLRQKGYVCGAGGEGEPAADPLHQMRRAAGDEFEFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGEPAADPLHQMRRAAGDEFEFRRT 60
 QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
 DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
 QY 121 QVQDMWVAVLETRLADVIHSSGMAEFTALYDGALEEARLRREGNMASTRVTLTGAVALL 180
 DB 121 QVQDMWVAVLETRLADVIHSSGMAEFTALYDGALEEARLRREGNMASTRVTLTGAVALL 180
 QY 181 GALVTVGAFPFASK 193
 DB 181 GALVTVGAFPFASK 193

RESULT 10
 AAY05532
 ID AAY05532 standard; protein; 193 AA.
 XX
 AC AAY05532;
 XX
 AC 05-JUL-1999 (first entry)
 DT
 XX
 DE Human Bcl-w protein essential for spermatogenesis.
 DE
 XX
 KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
 KW animal model.
 XX
 OS Homo sapiens.
 XX
 PN WO99137710-A1.

PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-AU000764.
 XX
 PR 16-SEP-1997; 97AU-00009228.
 XX
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX
 PI Cory S, Adams J, Print C, Gibson L, Koentgen F;
 DR WPI; 1999-243890/20.
 DR N-PSDB; AAX25134.
 XX
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
 PT protein associated with Bcl-w.
 PS
 XX Disclosure; Page 37; 52pp; English.
 XX
 CC The present sequence is described of a derivative of human Bcl-w (see
 CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely
 CC expressed and which is essential for spermatogenesis. The invention
 CC relates generally to a method of treatment and to an animal model for the
 CC identification of molecules and genetic sequences useful for inducing or
 CC reducing fertility of male animals. Methods are provided for the
 CC treatment of infertility, or for reducing fertility, by modulating
 CC spermatogenesis. An animal model carries a mutation is at least one
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules
 CC and are substantially infertile, but possess no other major abnormalities
 CC as determined by histological examination. They can be used to screen for
 CC therapeutic molecules including genetic sequences capable of inducing,
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which
 CC can induce infertility
 CC
 XX Sequence 193 AA;
 SQ
 Query Match 98.4%; Score 993; DB 2; Length 193;
 Best Local Similarity 97.9%; Pred. No. 4.2e-100;
 Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADVGVYKLRQKGYVCGAGGEGEPAADPLHQMRRAAGDEFEFRRT 60
 DB 1 MATPASAPDTRALVADVGVYKLRQKGYVCGAGGEGEPAADPLHQMRRAAGDEFEFRRT 60
 QY 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
 DB 61 FSDLAQLHTVTPGSAQGRFTQVSDLEFGGPNMGRVAFVFGAALCAESVNMKEPVLG 120
 QY 121 QVQDMWVAVLETRLADVIHSSGMAEFTALYDGALEEARLRREGNMASTRVTLTGAVALL 180
 DB 121 QVQDMWVAVLETRLADVIHSSGMAEFTALYDGALEEARLRREGNMASTRVTLTGAVALL 180
 QY 181 GALVTVGAFPFASK 193
 DB 181 GALVTVGAFPFASK 193

RESULT 11
 AAM97394
 ID AAM97394 standard; protein; 192 AA.
 XX
 AC AAM97394;
 XX
 AC 20-MAY-1999 (first entry)
 DT
 XX
 DE Mammalian bcl-y protein.
 DE
 XX
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
 KW premature cell death; cell death stimulator; prolonged cell life span;

| | | | |
|----|---|---|--|
| XX | 22-APR-1996 | (first entry) | |
| DT | | | |
| XX | Mouse bcl-w protein. | | |
| DE | | | |
| XX | Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; | | |
| KW | diagnosis; degenerative disease. | | |
| XX | | | |
| OS | Mus sp. | | |
| XX | | | |
| FN | W09735S971-A1. | | |
| XX | | | |
| PD | 02-OCT-1997. | | |
| XX | | | |
| PF | 27-MAR-1997; 97WO-AU000199. | | |
| XX | | | |
| PR | 27-MAR-1996; 96AU-00008965. | | |
| XX | | | |
| PA | (AMRA-) AMRAD OPERATIONS PTY LTD. | | |
| XX | | | |
| PI | Cory S, Adams JM, Gibson LM, Holmgren SP; | | |
| XX | | | |
| DR | WPI; 1997-489635/45. | | |
| XX | | | |
| DR | N-PSDB; AAT96578. | | |
| XX | | | |
| PT | Nucleic acid encoding apoptosis related gene bcl-w - used to induce or | | |
| PT | inhibit cell survival, e.g. for treatment of cancer and degenerative | | |
| XX | diseases. | | |
| PS | | | |
| XX | Claim 6; Page 50-51; 86pp; English. | | |
| XX | | | |
| CC | This sequence represents a novel protein, bcl-w, encoded by the mouse bcl | | |
| CC | -2 gene family. This gene promotes cell survival, so its modulation is | | |
| CC | useful in treatment of cancer or auto-immune diseases, degenerative | | |
| CC | diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular | | |
| CC | degeneration, hypoxia, ischaemia, human immunodeficiency virus infection | | |
| CC | or in cell transplants. Up-regulation of the gene can also be used to | | |
| CC | modify cell lines cultured in vivo, e.g. to develop new lines, to | | |
| CC | facilitate isolation of hybridomas and to increase survival of primary | | |
| CC | explants during genetic modification. It can be used to produce | | |
| CC | recombinant Bcl-w for therapy, diagnosis, antibody production or | | |
| CC | screening of potential modulators | | |
| XX | | | |
| SQ | Sequence 168 AA; | | |
| | | | |
| | Query Match | 86.8%; Score 876; DB 2; Length 168; | |
| | Best Local Similarity | 97.0%; Pred. No. 2.2e-87; | |
| | Matches | 163; Conservative 4; Mismatches 1; Indels 0; Gaps 0 | |
| OY | 1 NATPASTPDTRALVADFVGKYKLRQKGYCGAGPGSGPAPDPIHQAMRAAGDEFFTRPRT | 60 | |
| DB | 1 MPTPASTPDTRALVADFVGYRLRKQGYCGAGPGSGPAPDPIHQAMRAAGDEFFTRPRT | 60 | |
| OY | 61 FSDLLAQAHVTGSGAQRFTQVSDLPFGGPNWGLVAFVFGALCAESVVKEMEPVIG | 120 | |
| DB | 61 FSDLLAQAHVTGSGAQRFTQVSDLPFGGPNWGLVAFVFGALCAESVVKEMEPVIG | 120 | |
| OY | 121 QVQDMNVAVLEFTRLADWIIHSSGMAEFTALYDQGLIEARRLREGNWA | 168 | |
| DB | 121 QVQDMNVAVLEFTRLADWIIHSSGMAEFTALYDQGLIEARRLREGNWA | 168 | |
| | | | |
| | RESULT 14 | | |
| | AA018223 | | |
| | AA018223 standard; protein; 190 AA. | | |
| XX | AA018223; | | |
| AC | | | |
| XX | 18-SEP-2002 (first entry) | | |
| DT | | | |
| XX | | | |
| DE | Human Bcl-Rambo BHO domain related protein #4. | | |
| XX | | | |
| XX | Human; apoptotic signal transduction protein; Bcl-Rambo; BHO domain; | | |

| | | | |
|----|--|---|--|
| XX | OS | Unidentified. | |
| XX | PN | WO200248353-A2. | |
| XX | PD | 20-JUN-2002. | |
| XX | PF | 12-DEC-2001; 2001WO-EP014597. | |
| XX | PR | 12-DEC-2000; 2000DE-01061766. | |
| XX | PR | 04-JAN-2001; 2001DE-01000280. | |
| XX | PA | (APOT-) APOTECH RES & DEV LTD. | |
| XX | PI | Tschopp J, Hofmann K; | |
| XX | DR | WPI; 2002-537627/57. | |
| XX | PT | New DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors and for identifying therapeutic modulators of Bcl-Rambo function. | |
| XX | PS | Disclosure; Fig 1; 61pp; German. | |
| XX | CC | The present invention provides the protein and coding sequences of the human Bcl-Rambo apoptotic transcription factor, particularly the BHO domain. The sequences are useful in the treatment of diseases caused by | |
| XX | CC | incorrectly regulated intracellular signal transduction, including | |
| XX | CC | cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's diseases), muscular dystrophy, viral infections (including human | |
| XX | CC | immunodeficiency virus), autoimmune disease, septic shock, graft versus host disease and acute hepatitis. The present sequence is a protein | |
| XX | CC | described in the exemplification of the invention | |
| XX | SQ | Sequence 190 AA; | |
| XX | Query Match | 80.7%; Score 814.5; DB 5; Length 150; | |
| XX | Best Local Similarity | 87.0%; Pred. No. 1,4e-80; | |
| XX | Matches 168; Conservative | 1; Mismatches 21; Indels 3; Gaps 3; | |
| QY | 1 | MATPASTPDTRALVADFYGYTLRQKGYCGAGPGEPPADPLHQAMPBAGDEFTRFRRT 60 | |
| DB | 1 | MATPASABXTXAVAD-XGYTLRQKGYNGAGPGXGPAD-XHQXBAAGXEFTRFRRT 58 | |
| QY | 61 | FSDLAALQHLHTPGSAQORFTQVSEDLFQGGPNMRVLVAFFTFGALCAESYKMEPLVG 120 | |
| DB | 59 | FSDLAALQHLHTPGSAQORFTQVSEDLFQGGPNMRVLAFFTFGALCAESYKMEPLVG 118 | |
| QY | 121 | QVQDMMVAVYLETPLADWHSSGMAAEFTALYGDGALBPARLRKGNMVAVRTVLTGAVAL 180 | |
| DB | 119 | QXQEMVAVYLETPLAK-IHSSGMAAEFTALYGDGALBPARLRKGNMVAVRTVLTGAVAL 177 | |
| QY | 181 | GALVTVGAFPAK 193 | |
| DB | 178 | GALVTVGAFPAK 190 | |
| AC | AAW59884; | | |
| DT | 20-NOV-1998 | (First entry) | |
| DE | Amino acid sequence of the cDNA clone Bcl-1ike (HAICH29). | | |
| XX | Bcl-1ike (HAICH29); chronic inflammatory disease; allergic reaction; | | |
| XX | immunological disorder; autoimmune disease; anti-infectious agent. | | |
| KW | | | |

XX Homo sapiens.
 OS WO9831800-A2.
 XX 23-JUL-1998.
 XX
 XX 21-JAN-1998; 98WO-US000960.
 XX
 XX 21-JAN-1997; 97US-0034204P.
 PR 21-JAN-1997; 97US-0034205P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (AUCK-) AUCKLAND UNISERVICES LTD.
 XX
 PI Ni J, Rosen CA, Gentz RL, Feng P, Kristiansen GW, Su JY;
 XX
 DR WPI; 1998-414099/35.
 DR N-PSDB; AAV41925.
 XX
 XX New isolated polynucleotides and encoded polypeptides - used to develop
 PT products for treating e.g. inflammatory diseases, infections,
 PT immunological disorders, autoimmune diseases, allergies or tumours.
 XX
 PS Claim 1; Fig 12A-12D; 120pp; English.
 CC
 CC This is the amino acid sequence of the cDNA clone Bcl-1-like (HAICH29),
 CC used in the method of the invention. The products of the clone can be
 CC used for treating conditions associated with abnormal expression of the
 CC polypeptides. They can be used for e.g. treating chronic inflammatory
 CC diseases, immunological disorders, autoimmune diseases, inflammatory
 CC diseases, various allergies, and as anti-infectious agents. The products
 CC can also be used for detection and diagnosis
 CC
 SQ Sequence 365 AA;

Query Match 75.2%; Score 759; DB 2; Length 365;
 Best Local Similarity 98.6%; Pred. No. 3.9e-74;
 Matches 142; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTPTRALVADPFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEPFRFRRT 60
 Db 1 MATPASAPDPTRALVADPFGYKLRQKGYVCGAGPGEPPADPLHQAMRAAGDEPFRFRRT 60
 QY 61 FSDLAAGLHVTTPGSAQQRTQVSDLPFGGPNMGRIVAFFVFGALCAESVKNKEMEPVVG 120
 Db 61 FSDLAAGLHVTTPGSAQQRTQVSDLPFGGPNMGRIVAFFVFGALCAESVKNKEMEPVVG 120
 QY 121 QVQDMNVAVLETRLDADWIHSSGGW 144
 Db 121 QVQDMNVAVLETRLDADWIHSSGGW 144

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